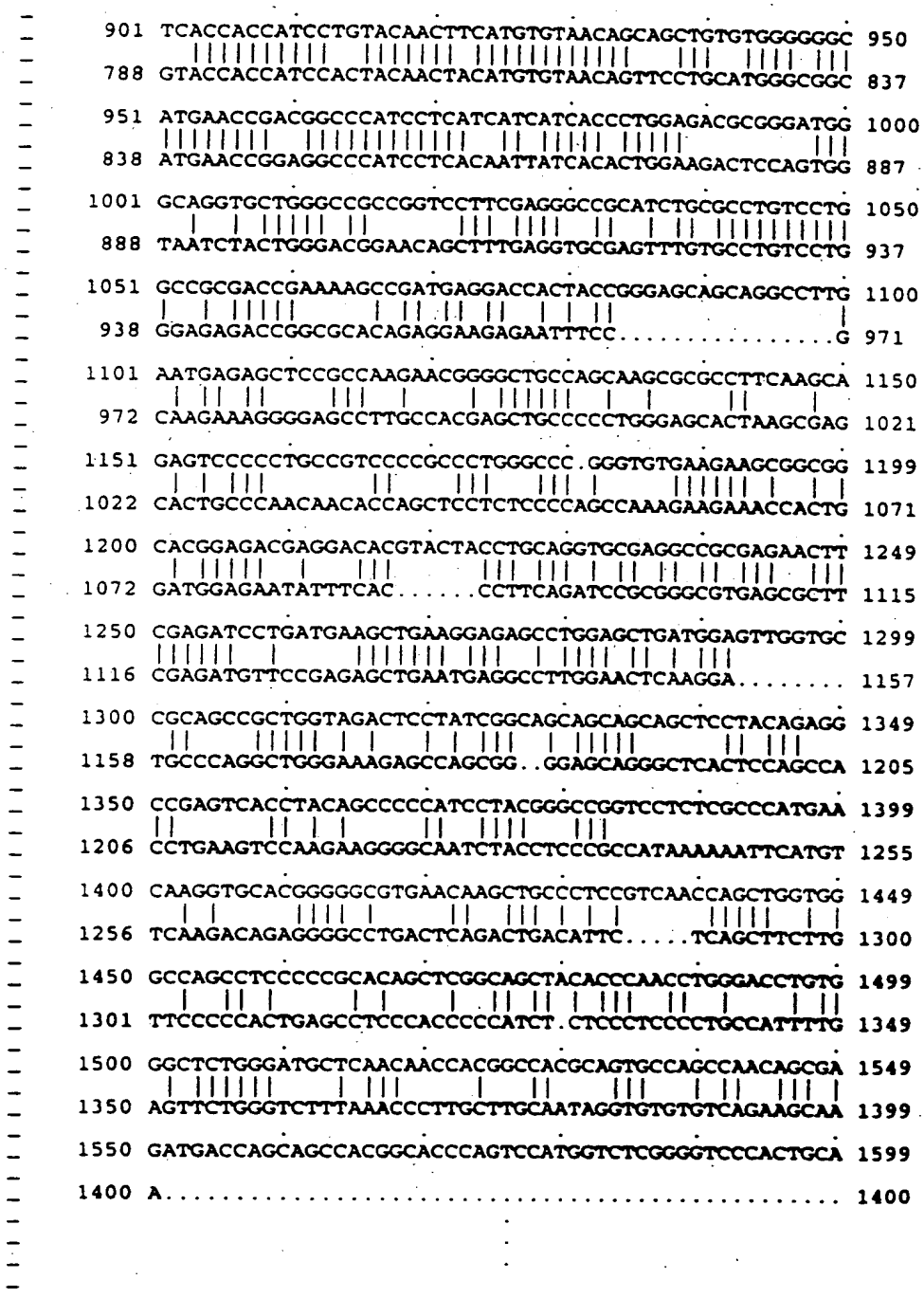
```
  1 TGCCTCCCCGCCCGCGCACCCGCCCCGAGGCCTGTGCTCCTGCGAAGGGG 50
                                                ||  ||||
  1 ..........................................GGGGCTCCGGGG 12

 51 ACGCAGCGAAGCCGGGGCCCGCGCCAGGCCGGCCGGGACGGACGCCGATG 100
    ||  |   |  |||||      ||  |     |  |   |     ||  |
 13 ACACTTGGCGTCCGGGCTGGAAGCGTGCTTTCCAAGACGGTGACACGCTT 62

101 CCCGGAGCTGCGACGGCTGCAGAGCGAGCTGCCCTCGGAGGCCGGTGTGA 150
    |||  |||     |  | ||   |  ||   |  |  |  |   |||   | |
 63 CCCTGAGGATTGGCAGCCAGACTGCTTACGGGTCAC...TGCCATGGAGG 109

151 GGAAGATGGCCCAGTCCACCACCACCTCCCCCGATGGGGGCACCACGTTT 200
      |   |  | |  |  |||  || |    ||||     |       || |||
110 AGCCGCAGTCAGATCCCAGCATCGAGCCCCCTCTGAGTCAGGAAACATTT 159

201 GAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACTTCGACCTTCC 250
       ||||  ||||      ||       | |||  |    |   ||  |||| |
160 TCAGACCTATGGAAACTACTTCCTGAAAACAAC.GTTCTGTCCCCCTTGC 208

251 CCAGTCAAGCCGGGGGAATAATGAGGTGGTGGGTGGCACGGATTCCAGCA 300
    |     |||||  | ||      |||  |   |    ||      || ||  |
209 CGTCCCAAGCGGTGGATGATTTGATGCTCTCTCCGGATGATCTTGCACAA 258

301 TGGACGTCTTCCACCTAGAGGGCATGACCACATCTGTCATGGCCCAGTTC 350
    |||                                 |   | | |  |||||  ||
259 TGG.........................TTAACTGAAGACCCAGGTC 280

351 AATTTGCTGAGCAGCACCATGGACCAGATGAGCAGCCGCGCTGCCTCGGC 400
      |  ||  |  |             |||||   |||  ||   || |
281 CAGATGAAGCTC...........CCAGAATGTCAGAGGCTGCTCCCCACA 319

401 CAGCCCGTACACCCCGGAGCACGCCGCCAGCGTGCCCACCCATTCACCCT 450
     ||||  |||||          |  | || |||  |||  |      |||
320 TGGCCCCCACACCAGCAGCTCCTACACCGGCGGCCCCTGCACCAGCCCC. 368

451 ACGCACAGCCCAGCTCCACCTTCGACACCATGTCGCCCGCGCCTGTCATC 500
                              | ||  | | |   |  |     ||
369 .........................CTCCTGGCCCCTGTCATCCTCTGTC 393

501 CCCTCCAACACCGACTATCCCGGACCCCACCACTTCGAGGTCACTTTCCA 550
    ||  |||  | |     |||  | |||    | ||    |||      |  ||||
394 CCTTCCCAGAAAACCTACCACGGCAGCTACGGTTTCCGTCTGGGCTTCCT 443

551 GCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCACTCTTGA 600
    |||  ||   |  ||  |||||||||  |   ||  ||  ||||||||||||     | | |
444 GCATTCTGGAACAGCCAAGTCTGTGACTTGCACGTACTCCCCTGACCTCA 493

601 AGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTG 650
    | ||  |  |  ||||||  | ||||||||  ||||||  | |||  |   |||
494 ACAAGATGTTTTGCCAGCTGGCCAAGACCTGCCCCGTGCAGCTGTGGGTT 543

651 TCCGCCCCACCGCCCCCGGGCACCGCCATCCGGGCCATGCCTGTCTACAA 700
      ||  ||||  ||  ||  ||||  |   |  ||||  ||||||  |  ||||||||
544 GATTCCACACCCCCGCCCGGCAGCCGCGTCCGCGCCATGGCCATCTACAA 593

701 GAAGGCGGAGCACGTGACCGACATCGTGAAGCGCTGCCCCAACCACGAGC 750
    | ||  |  |||||  ||||  ||  ||||||  ||||||||||  ||||  ||||
594 GCAGTCACAGCACATGACTGAGGTCGTGAGGCGCTGCCCCCACCATGAGC 643

751 TCGGGAGGGACTTCAACGAAGGACAGTCTGCCCCAGCCAGCCACCTCATC 800
    | |    |||  | | | |           |||||  |     ||  ||  |||
644 GCTGCTCAGACAGCGATGGA......CTGGCCCCTCCTCAACATCTTATC 687

801 CGTGTGGAAGGCAATAATCTCTCGCAGTATGTGGACGACCCTGTCACCGG 850
    ||  |||||||| |||   |     |  |||||  |||  |||       |||
688 CGAGTGGAAGGAAATTTGCGTGTGGAGTATTCGGATGACAGAAACACTTT 737

851 CAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACAGAAT 900
      | ||  ||  ||  ||||||||||||||||||  ||   ||||  ||  | ||  |
738 TCGACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTTGGCTCTGACT 787
```

FIG.1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788 GTACCACCATCCACTACAACTACATGTGTAACAGTTCCTGCATGGGCGGC 837
951 ATGAACCGACGGCCCATCCTCATCATCATCACCCTGGAGACGCGGGATGG 1000
838 ATGAACCGGAGGCCCATCCTCACAATTATCACACTGGAAGACTCCAGTGG 887
1001 GCAGGTGCTGGGCCGCCGGTCCTTCGAGGGCCGCATCTGCGCCTGTCCTG 1050
888 TAATCTACTGGGACGGAACAGCTTTGAGGTGCGAGTTTGTGCCTGTCCTG 937
1051 GCCGCGACCGAAAAGCCGATGAGGACCACTACCGGGAGCAGCAGGCCTTG 1100
938 GGAGAGACCGGCGCACAGAGGAAGAGAATTTCC.....G 971
1101 AATGAGAGCTCCGCCAAGAACGGGGCTGCCAGCAAGCGCGCCTTCAAGCA 1150
972 CAAGAAAGGGGAGCCTTGCCACGAGCTGCCCCCTGGGAGCACTAAGCGAG 1021
1151 GAGTCCCCCTGCCGTCCCCGCCCTGGGCCC.GGGTGTGAAGAAGCGGCGG 1199
1022 CACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAGAAACCACTG 1071
1200 CACGGAGACGAGGACACGTACTACCTGCAGGTGCGAGGCCGCGAGAACTT 1249
1072 GATGGAGAATATTTCAC.....CCTTCAGATCCGCGGGCGTGAGCGCTT 1115
1250 CGAGATCCTGATGAAGCTGAAGGAGAGCCTGGAGCTGATGGAGTTGGTGC 1299
1116 CGAGATGTTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGA..... 1157
1300 CGCAGCCGCTGGTAGACTCCTATCGGCAGCAGCAGCAGCTCCTACAGAGG 1349
1158 TGCCCAGGCTGGGAAAGAGCCAGCGG..GGAGCAGGGCTCACTCCAGCCA 1205
1350 CCGAGTCACCTACAGCCCCCATCCTACGGGCCGGTCCTCTCGCCCATGAA 1399
1206 CCTGAAGTCCAAGAAGGGGCAATCTACCTCCCGCCATAAAAAATTCATGT 1255
1400 CAAGGTGCACGGGGGCGTGAACAAGCTGCCCTCCGTCAACCAGCTGGTGG 1449
1256 TCAAGACAGAGGGGCCTGACTCAGACTGACATTC.....TCAGCTTCTTG 1300
1450 GCCAGCCTCCCCCCGCACAGCTCGGCAGCTACACCCAACCTGGGACCTGTG 1499
1301 TTCCCCCACTGAGCCTCCCACCCCCATCT.CTCCCTCCCCTGCCATTTTG 1349
1500 GGCTCTGGGATGCTCAACAACCACGGCCACGCAGTGCCAGCCAACAGCGA 1549
1350 AGTTCTGGGTCTTTAAACCCTTGCTTGCAATAGGTGTGTGTCAGAAGCAA 1399
1550 GATGACCAGCAGCCACGGCACCCAGTCCATGGTCTCGGGGTCCCACTGCA 1599
1400 A..... 1400

FIG.1 cont.

```
  1 MAQSTTTSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMD 50
    ..|:::...:|. :|    :.|: || .  .:|| : . .. .:|
  1 .....MEEPQSDPSIEPPLS....QETFSDLWKLLPENNVLSPLPSQAVD 41

 51 VFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 100
     : |   ... :||:   ... |: ......|.. .|..||..|. .| :
 42 DLML...SPDDLAQWLTEDPGPDEAPRMSEAAPHMAPTPAAPTPA.APAP 87

101 QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 150
    .||..:     .. :||...|.|.. | :.| :|:|||||.| |||| |.|
 88 APSWPL.....SSSVPSQKTYHGSYGFRLGFLHSGTAKSVTCTYSPDLNK 132

151 LYCQIAKTCPIQIKVSAPPPPGTAIRAMPVYKKAEHVTDIVKRCPNHELG 200
    ::||:|||||:|:.|...|||| .:|||::||..:|:|::|:|||:||
133 MFCQLAKTCPVQLWVDSTPPPGSRVRAMAIYKQSQHMTEVVRRCPHHE.. 180

201 RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 250
    |  :.:. ||: |||||||    :| ||. | |:||||||||:||.: |
181 RCSDSDGLAPPQHLIRVEGNLRVEYSDDRNTFRHSVVVPYEPPEVGSDCT 230

251 TILYNFMCNSSCVGGMNRRPILIIITLETRDGQVLGRRSFEGRICACPGR 300
    || ||:|||||:|||||||||.|||||...|.:|||.|||.|:||||||
231 TIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGR 280

301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHG 350
    ||:.:|:::|...  :.: .  .:..|||:..... |.    .|::.
281 DRRTEEENFRKKG..EPCHELPPGSTKRALPNNTSSSPQ.....PKKKPL 323

351 DEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPS 400
    |:: : ||:|||||.||:..|.|.|||.:  :.. ..: |.:   |....
324 DGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPAGSRAHSSHLKSKK 373

401 HLQPPSYGPVLSPMNKVHGGVNKLPSVNQLVGQPPPHSSAATPNLGPVGS 450
     .... ..: . : ..::
374 GQSTSRHKKFMFKTEGPDSD..............................  393
```

FIG. 2

```
  1 TGCCTCCCCGCCCGCGCACCCGCCCCGAGGCCTGTGCTCCTGCGAAGGGG 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 TGCCTCCCCGCCCGCGCACCCGCCCCGAGGCCTGTGCTCCTGCGAAGGGG 50

 51 ACGCAGCGAAGCCGGGGCCCCGCGCCAGGCCGGCCGGGACGGACGCCGATG 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 ACGCAGCGAAGCCGGGGCCCCGCGCCAGGCCGGCCGGGACGGACGCCGATG 100

101 CCCGGAGCTGCGACGGCTGCAGAGCGAGCTGCCCTCGGAGGCCGGTGTGA 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 CCCGGAGCTGCGACGGCTGCAGAGCGAGCTGCCCTCGGAGGCCGGTGTGA 150

151 GGAAGATGGCCCAGTCCACCACCACCTCCCCCGATGGGGGCACCACGTTT 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 GGAAGATGGCCCAGTCCACCACCACCTCCCCCGATGGGGGCACCACGTTT 200

201 GAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACTTCGACCTTCC 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 GAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACTTCGACCTTCC 250

251 CCAGTCAAGCCGGGGGGAATAATGAGGTGGTGGGTGGCACGGATTCCAGCA 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 CCAGTCAAGCCGGGGGGAATAATGAGGTGGTGGGTGGCACGGATTCCAGCA 300

301 TGGACGTCTTCCACCTAGAGGGCATGACCACATCTGTCATGGCCCAGTTC 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGGACGTCTTCCACCTAGAGGGCATGACCACATCTGTCATGGCCCAGTTC 350

351 AATTTGCTGAGCAGCACCATGGACCAGATGAGCAGCCGCGCTGCCTCGGC 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 AATTTGCTGAGCAGCACCATGGACCAGATGAGCAGCCGCGCTGCCTCGGC 400

401 CAGCCCGTACACCCCGGAGCACGCCGCCAGCGTGCCCACCCATTCACCCT 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 CAGCCCGTACACCCCGGAGCACGCCGCCAGCGTGCCCACCCATTCACCCT 450

451 ACGCACAGCCCAGCTCCACCTTCGACACCATGTCGCCCCGCGCCTGTCATC 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 ACGCACAGCCCAGCTCCACCTTCGACACCATGTCGCCCCGCGCCTGTCATC 500

501 CCCTCCAACACCGACTATCCCCGGACCCCACCACTTCGAGGTCACTTTCCA 550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 CCCTCCAACACCGACTATCCCCGGACCCCACCACTTCGAGGTCACTTTCCA 550

551 GCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCACTCTTGA 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
551 GCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCACTCTTGA 600

601 AGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTG 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
601 AGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTG 650

651 TCCGCCCCCACCGCCCCCGGGCACCGCCATCCGGGCCATGCCTGTCTACAA 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
651 TCCGCCCCCACCGCCCCCGGGCACCGCCATCCGGGCCATGCCTGTCTACAA 700

701 GAAGGCGGAGCACGTGACCGACATCGTGAAGCGCTGCCCCAACCACGAGC 750
    ||||||||||||||||||||||||||||||||||||||||||||||||||
701 GAAGGCGGAGCACGTGACCGACATCGTGAAGCGCTGCCCCAACCACGAGC 750

751 TCGGGAGGGACTTCAACGAAGGACAGTCTGCCCCAGCCAGCCACCTCATC 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 TCGGGAGGGACTTCAACGAAGGACAGTCTGCCCCAGCCAGCCACCTCATC 800

801 CGTGTGGAAGGCAATAATCTCTCGCAGTATGTGGACGACCCTGTCACCGG 850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
801 CGTGTGGAAGGCAATAATCTCTCGCAGTATGTGGACGACCCTGTCACCGG 850

851 CAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACAGAAT 900
    ||||||||||||||||||||||||||||||||||||||||||||||||||
851 CAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACAGAAT 900
```

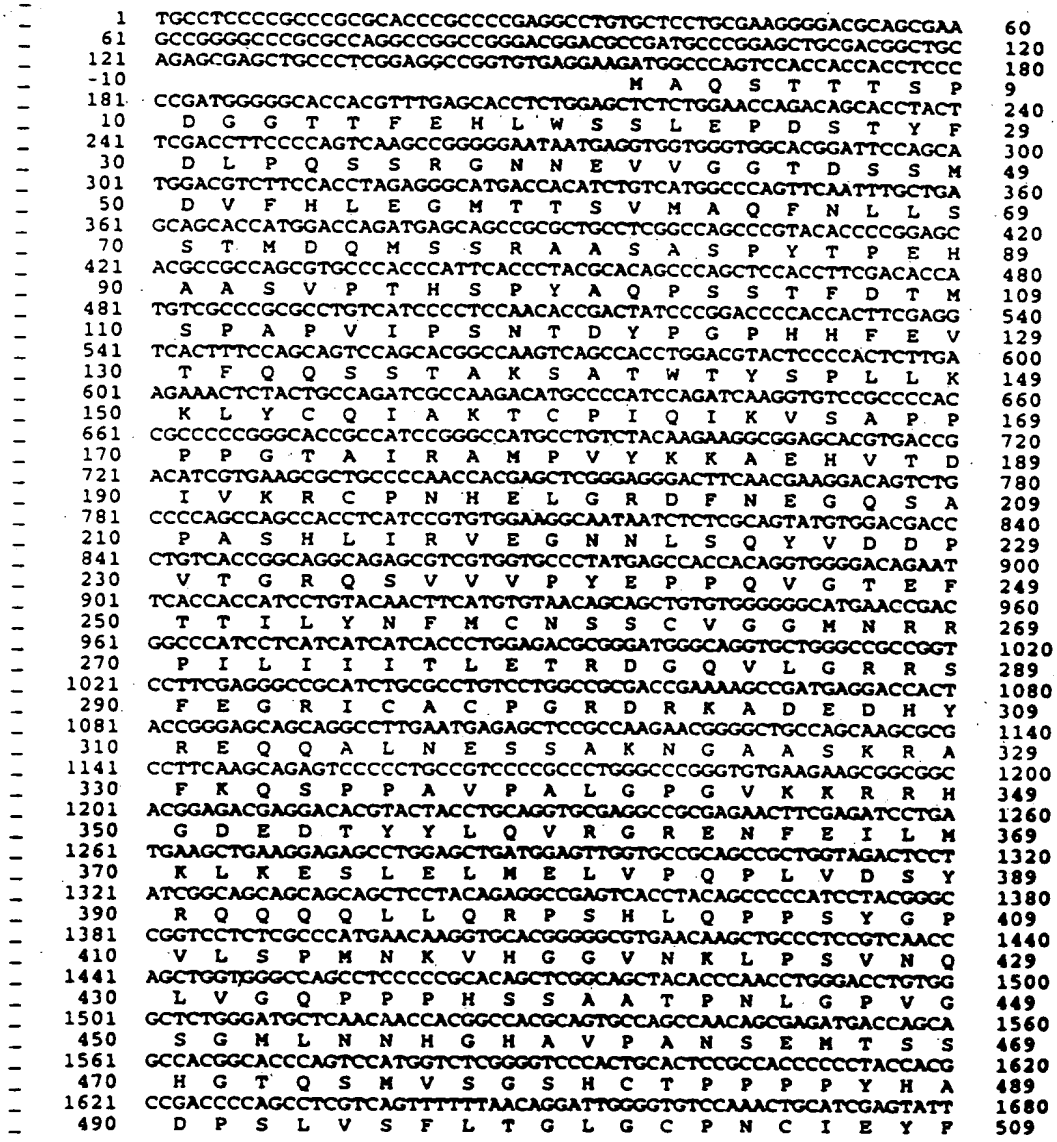
FIG.3 cont.

```
 901 TCACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTGGGGGGC 950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 901 TCACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTGGGGGGC 950

 951 ATGAACCGACGGCCCATCCTCATCATCATCACCCTGGAGACGCGGGATGG 1000
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 951 ATGAACCGACGGCCCATCCTCATCATCATCACCCTGGAGACGCGGGATGG 1000

1001 GCAGGTGCTGGGCCGCCGGTCCTTCGAGGGCCGCATCTGCGCCTGTCCTG 1050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1001 GCAGGTGCTGGGCCGCCGGTCCTTCGAGGGCCGCATCTGCGCCTGTCCTG 1050

1051 GCCGCGACCGAAAAGCCGATGAGGACCACTACCGGGAGCAGCAGGCCTTG 1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1051 GCCGCGACCGAAAAGCCGATGAGGACCACTACCGGGAGCAGCAGGCCTTG 1100

1101 AATGAGAGCTCCGCCAAGAACGGGGCTGCCAGCAAGCGCGCCTTCAAGCA 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1101 AATGAGAGCTCCGCCAAGAACGGGGCTGCCAGCAAGCGCGCCTTCAAGCA 1150

1151 GAGTCCCCCTGCCGTCCCCGCCCTGGGCCCGGGTGTGAAGAAGCGGCGGC 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1151 GAGTCCCCCTGCCGTCCCCGCCCTGGGCCCGGGTGTGAAGAAGCGGCGGC 1200

1201 ACGGAGACGAGGACACGTACTACCTGCAGGTGCGAGGCCGCGAGAACTTC 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1201 ACGGAGACGAGGACACGTACTACCTGCAGGTGCGAGGCCGCGAGAACTTC 1250

1251 GAGATCCTGATGAAGCTGAAGGAGAGCCTGGAGCTGATGGAGTTGGTGCC 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1251 GAGATCCTGATGAAGCTGAAGGAGAGCCTGGAGCTGATGGAGTTGGTGCC 1300

1301 GCAGCCGCTGGTAGACTCCTATCGGCAGCAGCAGCAGCTCCTACAGAGGC 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1301 GCAGCCGCTGGTAGACTCCTATCGGCAGCAGCAGCAGCTCCTACAGAGGC 1350

1351 CGAGTCACCTACAGCCCCCATCCTACGGGCCGGTCCTCTCGCCCATGAAC 1400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1351 CGAGTCACCTACAGCCCCCATCCTACGGGCCGGTCCTCTCGCCCATGAAC 1400

1401 AAGGTGCACGGGGGCGTGAACAAGCTGCCCTCCGTCAACCAGCTGGTGGG 1450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1401 AAGGTGCACGGGGGCGTGAACAAGCTGCCCTCCGTCAACCAGCTGGTGGG 1450

1451 CCAGCCTCCCCCCGCACAGCTCGGCAGCTACACCCAACCTGGGACCTGTGG 1500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1451 CCAGCCTCCCCCCGCACAGCTCGGCAGCTACACCCAACCTGGGACCTGTGG 1500

1501 GCTCTGGGATGCTCAACAACCACGGCCACGCAGTGCCAGCCAACAGCGAG 1550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1501 GCTCTGGGATGCTCAACAACCACGGCCACGCAGTGCCAGCCAACAGCGAG 1550

1551 ATGACCAGCAGCCACGGCACCCAGTCCATGGTCTCGGGGTCCCACTGCAC 1600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1551 ATGACCAGCAGCCACGGCACCCAGTCCATGGTCTCGGGGTCCCACTGCAC 1600

1601 TCCGCCACCCCCCTACCACGCCGACCCCAGCCTCGTCAGTTTTTTAACAG 1650
     ||||||||||||||||||||||||||||||||||||
1601 TCCGCCACCCCCCTACCACGCCGACCCCAGCCTCGTC..............  1637


1701 AGCATTTACCACCTGCAGAACCTGACCATCGAGGACCTGGGGGCCCTGAA 1750
                                 ||||||||||||||||||||
1638 ..............................AGGACCTGGGGGCCCTGAA 1656

1751 GATCCCCGAGCAGTATCGCATGACCATCTGGCGGGGCCTGCAGGACCTGA 1800
     ||||||||||||||||||||||||||||||||||||||||||||||||||
```

FIG.3 cont.

```
1657 GATCCCCGAGCAGTATCGCATGACCATCTGGCGGGGCCTGCAGGACCTGA 1706

1801 AGCAGGGCCACGACTACGGCGCCGCCGCGCAGCAGCTGCTCCGCTCCAGC 1850
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1707 AGCAGGGCCACGACTACGGCGCCGCCGCGCAGCAGCTGCTCCGCTCCAGC 1756

1851 AACGCGGCCGCCATTTCCATCGGCGGCTCCGGGGAGCTGCAGCGCCAGCG 1900
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1757 AACGCGGCCGCCATTTCCATCGGCGGCTCCGGGGAGCTGCAGCGCCAGCG 1806

1901 GGTCATGGAGGCCGTGCACTTCCGCGTGCGCCACACCATCACCATCCCCA 1950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1807 GGTCATGGAGGCCGTGCACTTCCGCGTGCGCCACACCATCACCATCCCCA 1856

1951 ACCGCGGCGGCCCCCGGCGCCGGCCCCGACGAGTGGGCGGACTTCGGCTTC 2000
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1857 ACCGCGGCGGCCCCCGGCGCCGGCCCCGACGAGTGGGCGGACTTCGGCTTC 1906

2001 GACCTGCCCCGACTGCAAGGCCCGCAAGCAGCCCATCAAGGAGGAGTTCAC 2050
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1907 GACCTGCCCGACTGCAAGGCCCGCAAGCAGCCCATCAAGGAGGAGTTCAC 1956

2051 GGAGGCCGAGATCCACTGAGGGGCCGGGCCCAGCCAGAGCCTGTGCCACC 2100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1957 GGAGGCCGAGATCCACTGAGGGGCCGGGCCCAGCCAGAGCCTGTGCCACC 2006

2101 GCCCAGAGACCCAGGCCGCCTCGCTCTC 2128
     ||||||||||||||||||||||||||||
2007 GCCCAGAGACCCAGGCCGCCTCGCTCTC 2034
```

FIG. 3 cont.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61 GCCGGGGCCCGCGCCAGGCCGGCCGGGACGGACGCCGATGCCCGGAGCTGCGACGGCTGC 120
121 AGAGCGAGCTGCCCTCGGAGGCCGGTGTGAGGAAGATGGCCCAGTCCACCACCACCTCCC 180
-10 M A Q S T T T S P
181 CCGATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACT 240
10 D G G T T F E H L W S S L E P D S T Y F 29
241 TCGACCTTCCCCAGTCAAGCCGGGGGAATAATGAGGTGGTGGGTGGCACGGATTCCAGCA 300
30 D L P Q S S R G N N E V V G G T D S S M 49
301 TGGACGTCTTCCACCTAGAGGGCATGACCACATCTGTCATGGCCCAGTTCAATTTGCTGA 360
50 D V F H L E G M T T S V M A Q F N L L S 69
361 GCAGCACCATGGACCAGATGAGCAGCCGCGCTGCCTCGGCCAGCCCGTACACCCCGGAGC 420
70 S T M D Q M S S R A A S A S P Y T P E H 89
421 ACGCCGCCAGCGTGCCCACCCATTCACCCTACGCACAGCCCAGCTCCACCTTCGACACCA 480
90 A A S V P T H S P Y A Q P S S T F D T M 109
481 TGTCGCCCGCGCCTGTCATCCCCTCCAACACCGACTATCCCGGACCCCACCACTTCGAGG 540
110 S P A P V I P S N T D Y P G P H H F E V 129
541 TCACTTTCCAGCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCACTCTTGA 600
130 T F Q Q S S T A K S A T W T Y S P L L K 149
601 AGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCGCCCCAC 660
150 K L Y C Q I A K T C P I Q I K V S A P P 169
661 CGCCCCCGGGCACCGCCATCCGGGCCATGCCTGTCTACAAGAAGGCGGAGCACGTGACCG 720
170 P P G T A I R A M P V Y K K A E H V T D 189
721 ACATCGTGAAGCGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACGAAGGACAGTCTG 780
190 I V K R C P N H E L G R D F N E G Q S A 209
781 CCCCAGCCAGCCACCTCATCCGTGTGGAAGGCAATAATCTCTCGCAGTATGTGGACGACC 840
210 P A S H L I R V E G N N L S Q Y V D D P 229
841 CTGTCACCGGCAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACAGAAT 900
230 V T G R Q S V V V P Y E P P Q V G T E F 249
901 TCACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTGGGGGGCATGAACCGAC 960
250 T T I L Y N F M C N S S C V G G M N R R 269
961 GGCCCATCCTCATCATCATCACCCTGGAGACGCGGGATGGGCAGGTGCTGGGCCGCCGGT 1020
270 P I L I I I T L E T R D G Q V L G R R S 289
1021 CCTTCGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCCGATGAGGACCACT 1080
290 F E G R I C A C P G R D R K A D E D H Y 309
1081 ACCGGGAGCAGCAGGCCTTGAATGAGAGCTCCGCCAAGAACGGGGCTGCCAGCAAGCGCG 1140
310 R E Q Q A L N E S S A K N G A A S K R A 329
1141 CCTTCAAGCAGAGTCCCCCTGCCGTCCCCGCCCTGGGCCCGGGTGTGAAGAAGCGGCGGC 1200
330 F K Q S P P A V P A L G P G V K K R R H 349
1201 ACGGAGACGAGGACACGTACTACCTGCAGGTGCGAGGCCGCGAGAACTTCGAGATCCTGA 1260
350 G D E D T Y Y L Q V R G R E N F E I L M 369
1261 TGAAGCTGAAGGAGAGCCTGGAGCTGATGGAGTTGGTGCCGCAGCCGCTGGTAGACTCCT 1320
370 K L K E S L E L M E L V P Q P L V D S Y 389
1321 ATCGGCAGCAGCAGCAGCTCCTACAGAGGCCGAGTCACCTACAGCCCCCATCCTACGGGC 1380
390 R Q Q Q Q L L Q R P S H L Q P P S Y G P 409
1381 CGGTCCTCTCGCCCATGAACAAGGTGCACGGGGGCGTGAACAAGCTGCCCTCCGTCAACC 1440
410 V L S P M N K V H G G V N K L P S V N Q 429
1441 AGCTGGTGGGCCAGCCTCCCCCGCACAGCTCGGCAGCTACACCCAACCTGGGACCTGTGG 1500
430 L V G Q P P P H S S A A T P N L G P V G 449
1501 GCTCTGGGATGCTCAACAACCACGGCCACGCAGTGCCAGCCAACAGCGAGATGACCAGCA 1560
450 S G M L N N H G H A V P A N S E M T S S 469
1561 GCCACGGCACCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCACG 1620
470 H G T Q S M V S G S H C T P P P P Y H A 489
1621 CCGACCCCAGCCTCGTCAGTTTTTTAACAGGATTGGGGTGTCCAAACTGCATCGAGTATT 1680
490 D P S L V S F L T G L G C P N C I E Y F 509

FIG.4

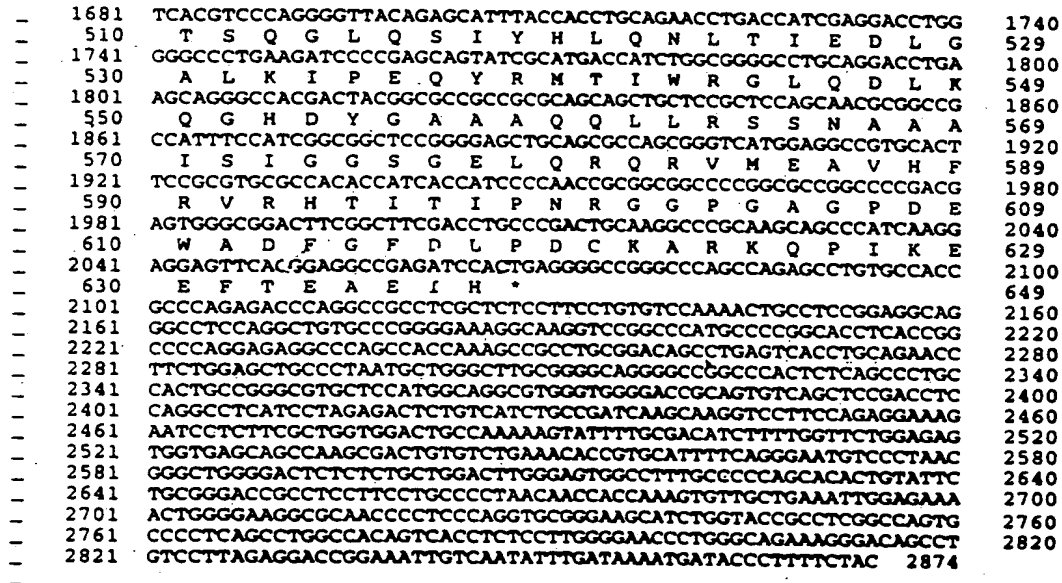
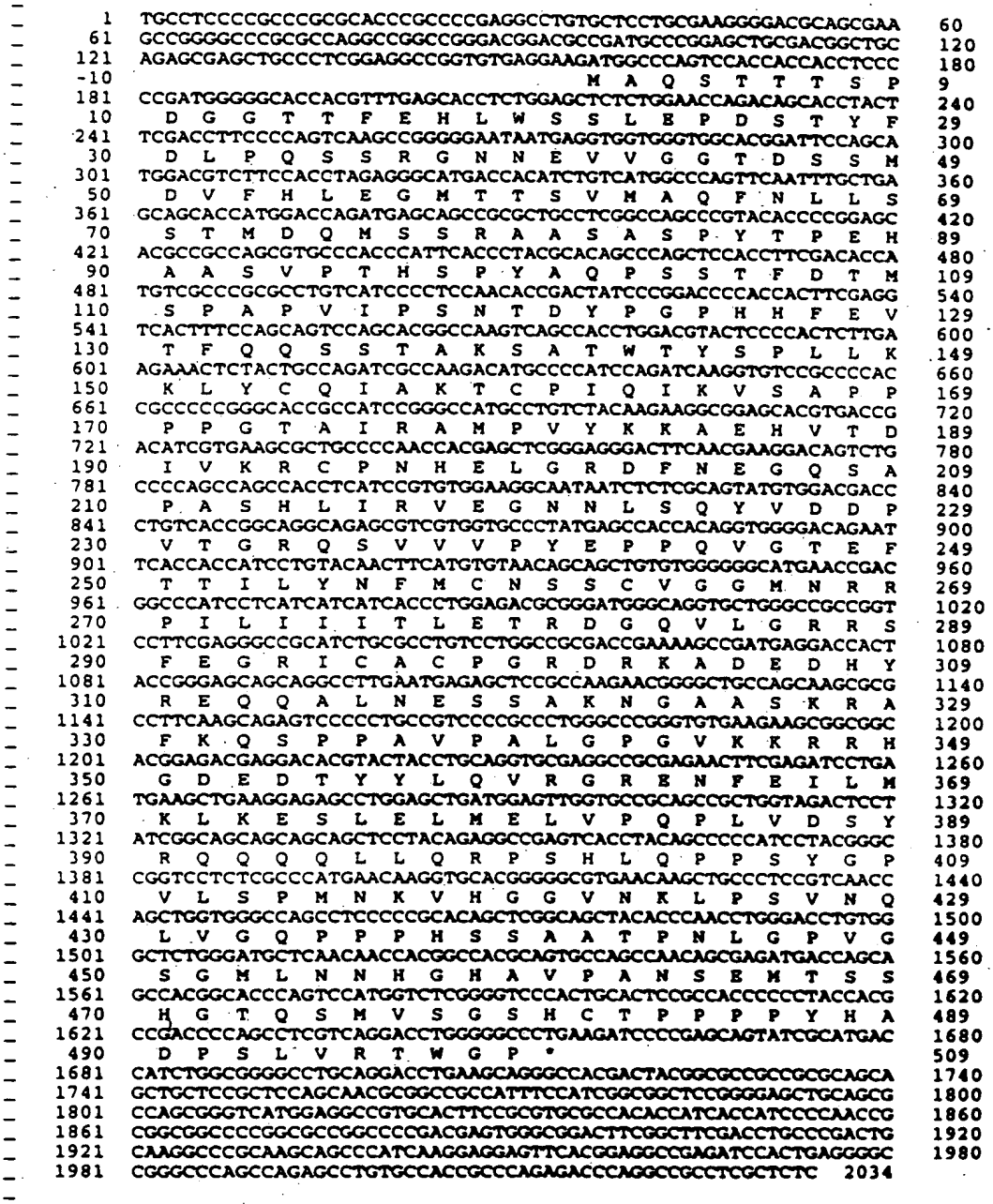

1681 TCACGTCCCAGGGGTTACAGAGCATTTACCACCTGCAGAACCTGACCATCGAGGACCTGG 1740
510 T S Q G L Q S I Y H L Q N L T I E D L G 529
1741 GGGCCCTGAAGATCCCCGAGCAGTATCGCATGACCATCTGGCGGGGCCTGCAGGACCTGA 1800
530 A L K I P E Q Y R M T I W R G L Q D L K 549
1801 AGCAGGGCCACGACTACGGCGCCGCCGCGCAGCAGCTGCTCCGCTCCAGCAACGCGGCCG 1860
550 Q G H D Y G A A A Q Q L L R S S N A A A 569
1861 CCATTTCCATCGGCGGCTCCGGGGAGCTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACT 1920
570 I S I G G S G E L Q R Q R V M E A V H F 589
1921 TCCGCGTGCGCCACACCATCACCATCCCCAACCGCGGCGGCCCCGGCGCCGGCCCCGACG 1980
590 R V R H T I T I P N R G G P G A G P D E 609
1981 AGTGGGCGGACTTCGGCTTCGACCTGCCCGACTGCAAGGCCCGCAAGCAGCCCATCAAGG 2040
610 W A D F G F D L P D C K A R K Q P I K E 629
2041 AGGAGTTCACGGAGGCCGAGATCCACTGAGGGGCCGGGCCCAGCCAGAGCCTGTGCCACC 2100
630 E F T E A E I H * 649
2101 GCCCAGAGACCCAGGCCGCCTCGCTCTCCTTCCTGTGTCCAAAACTGCCTCCGGAGGCAG 2160
2161 GGCCTCCAGGCTGTGCCCGGGGAAAGGCAAGGTCCGGCCCATGCCCCGGCACCTCACCGG 2220
2221 CCCCAGGAGAGGCCCAGCCACCAAAGCCGCCTGCGGACAGCCTGAGTCACCTGCAGAACC 2280
2281 TTCTGGAGCTGCCCTAATGCTGGGCTTGCGGGGCAGGGGCCGGCCCACTCTCAGCCCTGC 2340
2341 CACTGCCGGGCGTGCTCCATGGCAGGCGTGGGTGGGGACCGCAGTGTCAGCTCCGACCTC 2400
2401 CAGGCCTCATCCTAGAGACTCTGTCATCTGCCGATCAAGCAAGGTCCTTCCAGAGGAAAG 2460
2461 AATCCTCTTCGCTGGTGGACTGCCAAAAAGTATTTTGCGACATCTTTTGGTTCTGGAGAG 2520
2521 TGGTGAGCAGCCAAGCGACTGTGTCTGAAACACCGTGCATTTTCAGGGAATGTCCCTAAC 2580
2581 GGGCTGGGGACTCTCTCTGCTGGACTTGGGAGTGGCCTTTGCCCCCAGCACACTGTATTC 2640
2641 TGCGGGACCGCCTCCTTCCTGCCCCTAACAACCACCAAAGTGTTGCTGAAATTGGAGAAA 2700
2701 ACTGGGGAAGGCGCAACCCCTCCCAGGTGCGGGAAGCATCTGGTACCGCCTCGGCCAGTG 2760
2761 CCCCTCAGCCTGGCCACAGTCACCTCTCCTTGGGGAACCCTGGGCAGAAAGGGACAGCCT 2820
2821 GTCCTTAGAGGACCGGAAATTGTCAATATTTGATAAAATGATACCCTTTTCTAC 2874

FIG.4 cont.



```
     1  TGCCTCCCCGCCCGCGCACCCGCCCCGAGGCCTGTGCTCCTGCGAAGGGGACGCAGCGAA   60
    61  GCCGGGGCCCGCGCCAGGCCGGCCGGGACGGACGCCGATGCCCGGAGCTGCGACGGCTGC  120
   121  AGAGCGAGCTGCCCTCGGAGGCCGGTGTGAGGAAGATGGCCCAGTCCACCACCACCTCCC  180
   -10                                    M  A  Q  S  T  T  T  S  P    9
   181  CCGATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACT  240
    10    D  G  G  T  T  F  E  H  L  W  S  S  L  E  P  D  S  T  Y  F   29
   241  TCGACCTTCCCCAGTCAAGCCGGGGGAATAATGAGGTGGTGGGTGGCACGGATTCCAGCA  300
    30    D  L  P  Q  S  S  R  G  N  N  E  V  V  G  G  T  D  S  S  M   49
   301  TGGACGTCTTCCACCTAGAGGGCATGACCACATCTGTCATGGCCCAGTTCAATTTGCTGA  360
    50    D  V  F  H  L  E  G  M  T  T  S  V  M  A  Q  F  N  L  L  S   69
   361  GCAGCACCATGGACCAGATGAGCAGCCGCGCTGCCTCGGCCAGCCCGTACACCCCGGAGC  420
    70    S  T  M  D  Q  M  S  S  R  A  A  S  A  S  P  Y  T  P  E  H   89
   421  ACGCCGCCAGCGTGCCCACCCATTCACCCTACGCACAGCCCAGCTCCACCTTCGACACCA  480
    90    A  A  S  V  P  T  H  S  P  Y  A  Q  P  S  S  T  F  D  T  M  109
   481  TGTCGCCCGCGCCTGTCATCCCCTCCAACACCGACTATCCCGGACCCCACCACTTCGAGG  540
   110    S  P  A  P  V  I  P  S  N  T  D  Y  P  G  P  H  H  F  E  V  129
   541  TCACTTTCCAGCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCACTCTTGA  600
   130    T  F  Q  Q  S  S  T  A  K  S  A  T  W  T  Y  S  P  L  L  K  149
   601  AGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCGCCCCAC  660
   150    K  L  Y  C  Q  I  A  K  T  C  P  I  Q  I  K  V  S  A  P  P  169
   661  CGCCCCCGGGCACCGCCATCCGGGCCATGCCTGTCTACAAGAAGGCGGAGCACGTGACCG  720
   170    P  P  G  T  A  I  R  A  M  P  V  Y  K  K  A  E  H  V  T  D  189
   721  ACATCGTGAAGCGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACGAAGGACAGTCTG  780
   190    I  V  K  R  C  P  N  H  E  L  G  R  D  F  N  E  G  Q  S  A  209
   781  CCCCAGCCAGCCACCTCATCCGTGTGGAAGGCAATAATCTCTCGCAGTATGTGGACGACC  840
   210    P  A  S  H  L  I  R  V  E  G  N  N  L  S  Q  Y  V  D  D  P  229
   841  CTGTCACCGGCAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACAGAAT  900
   230    V  T  G  R  Q  S  V  V  V  P  Y  E  P  P  Q  V  G  T  E  F  249
   901  TCACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTGGGGGGCATGAACCGAC  960
   250    T  T  I  L  Y  N  F  M  C  N  S  S  C  V  G  G  M  N  R  R  269
   961  GGCCCATCCTCATCATCATCACCCTGGAGACGCGGGATGGGCAGGTGCTGGGCCGCCGGT 1020
   270    P  I  L  I  I  I  T  L  E  T  R  D  G  Q  V  L  G  R  R  S  289
  1021  CCTTCGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCCGATGAGGACCACT 1080
   290    F  E  G  R  I  C  A  C  P  G  R  D  R  K  A  D  E  D  H  Y  309
  1081  ACCGGGAGCAGCAGGCCTTGAATGAGAGCTCCGCCAAGAACGGGGCTGCCAGCAAGCGCG 1140
   310    R  E  Q  Q  A  L  N  E  S  S  A  K  N  G  A  A  S  K  R  A  329
  1141  CCTTCAAGCAGAGTCCCCCTGCCGTCCCCGCCCTGGGCCCGGGTGTGAAGAAGCGGCGGC 1200
   330    F  K  Q  S  P  P  A  V  P  A  L  G  P  G  V  K  K  R  R  H  349
  1201  ACGGAGACGAGGACACGTACTACCTGCAGGTGCGAGGCCGCGAGAACTTCGAGATCCTGA 1260
   350    G  D  E  D  T  Y  Y  L  Q  V  R  G  R  E  N  F  E  I  L  M  369
  1261  TGAAGCTGAAGGAGAGCCTGGAGCTGATGGAGTTGGTGCCGCAGCCGCTGGTAGACTCCT 1320
   370    K  L  K  E  S  L  E  L  M  E  L  V  P  Q  P  L  V  D  S  Y  389
  1321  ATCGGCAGCAGCAGCAGCTCCTACAGAGGCCGAGTCACCTACAGCCCCCATCCTACGGGC 1380
   390    R  Q  Q  Q  Q  L  L  Q  R  P  S  H  L  Q  P  P  S  Y  G  P  409
  1381  CGGTCCTCTCGCCCATGAACAAGGTGCACGGGGGCGTGAACAAGCTGCCCTCCGTCAACC 1440
   410    V  L  S  P  M  N  K  V  H  G  G  V  N  K  L  P  S  V  N  Q  429
  1441  AGCTGGTGGGCCAGCCTCCCCCGCACAGCTCGGCAGCTACACCCAACCTGGGACCTGTGG 1500
   430    L  V  G  Q  P  P  P  H  S  S  A  A  T  P  N  L  G  P  V  G  449
  1501  GCTCTGGGATGCTCAACAACCACGGCCACGCAGTGCCAGCCAACAGCGAGATGACCAGCA 1560
   450    S  G  M  L  N  N  H  G  H  A  V  P  A  N  S  E  M  T  S  S  469
  1561  GCCACGGCACCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCACG 1620
   470    H  G  T  Q  S  M  V  S  G  S  H  C  T  P  P  P  P  Y  H  A  489
  1621  CCGACCCCAGCCTCGTCAGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTATCGCATGAC 1680
   490    D  P  S  L  V  R  T  W  G  P  *                            509
  1681  CATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACGGCGCCGCCGCGCAGCA 1740
  1741  GCTGCTCCGCTCCAGCAACGCGGCCGCCATTTCCATCGGCGGCTCCGGGGAGCTGCAGCG 1800
  1801  CCAGCGGGTCATGGAGGCCGTGCACTTCCGCGTGCGCCACACCATCACCATCCCCAACCG 1860
  1861  CGGCGGCCCCGGCGCCGGCCCCGACGAGTGGGCGGACTTCGGCTTCGACCTGCCCGACTG 1920
  1921  CAAGGCCCGCAAGCAGCCCATCAAGGAGGAGTTCACGGAGGCCGAGATCCACTGAGGGGC 1980
  1981  CGGGCCCAGCCAGAGCCTGTGCCACCGCCCAGAGACCCAGGCCGCCTCGCTCTC  2034
```

FIG.5

```
   1  GCGAGCTGCCCTCGGAGGCCGGCGTGGGGAAGATGGCCCAGTCCACCGCCACCTCCCCTG   60
  -9                                  M  A  Q  S  T  A  T  S  P  D   10
  61  ATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCTCTGGAACCAGACAGCACCTACTTCG  120
  11    G  G  T  T  F  E  H  L  W  S  S  L  E  P  D  S  T  Y  F  D   30
 121  ACCTTCCCCAGTCAAGCCGGGGGAATAATGAGGTGGTGGGCGGAACGGATTCCAGCATGG  180
  31    L  P  Q  S  S  R  G  N  N  E  V  V  G  G  T  D  S  S  M  D   50
 181  ACGTCTTCCACCTGGAGGGCATGACTACATCTGTCATGGCCCAGTTCAATCTGCTGAGCA  240
  51    V  F  H  L  E  G  M  T  T  S  V  M  A  Q  F  N  L  L  S  S   70
 241  GCACCATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGAGCACG  300
  71    T  M  D  Q  M  S  S  R  A  A  S  A  S  P  Y  T  P  E  H  A   90
 301  CCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCACCTTCGACACCATGT  360
  91    A  S  V  P  T  H  S  P  Y  A  Q  P  S  S  T  F  D  T  M  S  110
 361  CGCCGGCGCCTGTCATCCCCTCCAACACCGACTACCCCGGACCCCACCACTTTGAGGTCA  420
 111    P  A  P  V  I  P  S  N  T  D  Y  P  G  P  H  H  F  E  V  T  130
 421  CTTTCCAGCAGTCCAGCACGGCCAAGTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGA  480
 131    F  Q  Q  S  S  T  A  K  S  A  T  W  T  Y  S  P  L  L  K  K  150
 481  AACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCAC  540
 151    L  Y  C  Q  I  A  K  T  C  P  I  Q  I  K  V  S  T  P  P  P  170
 541  CCCCAGGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGACCGACG  600
 171    P  G  T  A  I  R  A  M  P  V  Y  K  K  A  E  H  V  T  D  V  190
 601  TCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACGAAGGACAGTCTGCTC  660
 191    V  K  R  C  P  N  H  E  L  G  R  D  F  N  E  G  Q  S  A  P  210
 661  CAGCCAGCCACCTCATCCGCGTGGAAGGCAATAATCTCTCGCAGTATGTGGATGACCCTG  720
 211    A  S  H  L  I  R  V  E  G  N  N  L  S  Q  Y  V  D  D  P  V  230
 721  TCACCGGCAGGCAGAGCGTCGTGGTGCCCTATGAGCCACCACAGGTGGGGACGGAATTCA  780
 231    T  G  R  Q  S  V  V  V  P  Y  E  P  P  Q  V  G  T  E  F  T  250
 781  CCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGC  840
 251    T  I  L  Y  N  F  M  C  N  S  S  C  V  G  G  M  N  R  R  P  270
 841  CCATCCTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCGGTCCT  900
 271    I  L  I  I  I  T  L  E  M  R  D  G  Q  V  L  G  R  R  S  F  290
 901  TTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTGATGAGGACCACTACC  960
 291    E  G  R  I  C  A  C  P  G  R  D  R  K  A  D  E  D  H  Y  R  310
 961  GGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAGAACGGGGCCGCCAGCAAGCGTGCCT 1020
 311    E  Q  Q  A  L  N  E  S  S  A  K  N  G  A  A  S  K  R  A  F  330
1021  TCAAGCAGAGCCCCCCTGCCGTCCCCGCCCTTGGTGCCGGTGTGAAGAAGCGGCGGCATG 1080
 331    K  Q  S  P  P  A  V  P  A  L  G  A  G  V  K  K  R  R  H  G  350
1081  GAGACGAGGACACGTACTACCTTCAGGTGCGAGGCCGGGAGAACTTTGAGATCCTGATGA 1140
 351    D  E  D  T  Y  Y  L  Q  V  R  G  R  E  N  F  E  I  L  M  K  370
1141  AGCTGAAAGAGAGCCTGGAGCTGATGGAGTTGGTGCCGCAGCCACTGGTGGACTCCTATC 1200
 371    L  K  E  S  L  E  L  M  E  L  V  P  Q  P  L  V  D  S  Y  R  390
1201  GGCAGCAGCAGCAGCTCCTACAGAGGCCGAGTCACCTACAGCCCCCGTCCTACGGGCCGG 1260
 391    Q  Q  Q  Q  L  L  Q  R  P  S  H  L  Q  P  P  S  Y  G  P  V  410
1261  TCCTCTCGCCCATGAACAAGGTGCACGGGGGCATGAACAAGCTGCCCTCCGTCAACCAGC 1320
 411    L  S  P  M  N  K  V  H  G  G  M  N  K  L  P  S  V  N  Q  L  430
1321  TGGTGGGCCAGCCTCCCCCGCACAGTTCGGCAGCTACACCCAACCTGGGGCCCGTGGGCC 1380
 431    V  G  Q  P  P  P  H  S  S  A  A  T  P  N  L  G  P  V  G  P  450
1381  CCGGGATGCTCAACAACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCC 1440
 451    G  M  L  N  N  H  G  H  A  V  P  A  N  G  E  M  S  S  S  H  470
```

FIG.6

```
1441  ACAGCGCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCACGCCG  1500
 471    S  A  Q  S  M  V  S  G  S  H  C  T  P  P  P  P  Y  H  A  D   490
1501  ACCCCAGCCTCGTCAGTTTTTTAACAGGATTGGGGTGTCCAAACTGCATCGAGTATTTCA  1560
 491    P  S  L  V  S  F  L  T  G  L  G  C  P  N  C  I  E  Y  F  T   510
1561  CCTCCCAAGGGTTACAGAGCATTTACCACCTGCAGAACCTGACCATTGAGGACCTGGGGG  1620
 511    S  Q  G  L  Q  S  I  Y  H  L  Q  N  L  T  I  E  D  L  G  A   530
1621  CCCTGAAGATCCCCGAGCAGTACCGCATGACCATCTGGCGGGGCCTGCAGGACCTGAAGC  1680
 531    L  K  I  P  E  Q  Y  R  M  T  I  W  R  G  L  Q  D  L  K  Q   550
1681  AGGGCCACGACTACAGCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCT  1740
 551    G  H  D  Y  S  T  A  Q  Q  L  L  R  S  S  N  A  A  T  I  S   570
1741  CCATCGGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTTCCGCG  1800
 571    I  G  G  S  G  E  L  Q  R  Q  R  V  M  E  A  V  H  F  R  V   590
1801  TGCGCCACACCATCACCATCCCCAACCGCGGCGGCCCAGGCGGCGGCCCTGACGAGTGGG  1860
 591    R  H  T  I  T  I  P  N  R  G  G  P  G  G  G  P  D  E  W  A   610
1861  CGGACTTCGGCTTCGACCTGCCCGACTGCAAGGCCCGCAAGCAGCCCATCAAGGAGGAGT  1920
 611    D  F  G  F  D  L  P  D  C  K  A  R  K  Q  P  I  K  E  E  F   630
1921  TCACGGAGGCCGAGATCCACTGAGGGCCTCGCCTGGCTGCAGCCTGCGCCACCGCCCAGA  1980
 631    T  E  A  E  I  H  *                                          650
1981  GACCCAAGCTGCCTCCCCTCTCCTTCCTGTGTGTCCAAAACTGCCTCAGGAGGCAGGACC  2040
2041  TTCGGGCTGTGCCCGGGGAAAGGCAAGGTCCGGCCCATCCCCAGGCACCTCACAGGCCCC  2100
2101  AGGAAAGGCCCAGCCACCGAAGCCGCCTGTGGACAGCCTGAGTCACCTGCAGAACC      2156
```

FIG.6 cont.

```
     1  TGATCTCCCTGTGGCCTGCAGGGGACTGAGCCAGGGAGTAGATGCCCTGAGACCCCAAGG   60
    61  GACACCCAAGGAAACCTTGCTGGCTTTGAGAAAGGGATCGTCTCTCTCCTGCCCAAGAGA  120
   121  AGCATGTGTATGGGCCCTGTGTATGAATCCTTGGGGCAGGCCCAGTTCAATTTGCTCAGC  180
     0     M  C  M  G  P  V  Y  E  S  L  G  Q  A  Q  F  N  L  L  S     19
   181  AGTGCCATGGACCAGATGGGCAGCCGTGCGGCCCCGGCGAGCCCCTACACCCCGGAGCAC  240
    20  S  A  M  D  Q  M  G  S  R  A  A  P  A  S  P  Y  T  P  E  H     39
   241  GCCGCCAGCGCGCCCACCCACTCGCCCTACGCGCAGCCCAGCTCCACCTTCGACACCATG  300
    40  A  A  S  A  P  T  H  S  P  Y  A  Q  P  S  S  T  F  D  T  M     59
   301  TCTCCGGCGCCTGTCATCCCTTCCAATACCGACTACCCCGGCCCCCACCCCTTCGAGGTC  360
    60  S  P  A  P  V  I  P  S  N  T  D  Y  P  G  P  H  H  F  E  V     79
   361  ACCTTCCAGCAGTCGAGCACTGCCAAGTCGGCCACCTGGACATACTCCCCACTCTTGAAG  420
    80  T  F  Q  Q  S  S  T  A  K  S  A  T  W  T  Y  S  P  L  L  K     99
   421  AAGTTGTACTGTCAGATTGCTAAGACATGCCCCATCCAGATCAAAGTGTCCACACCACCA  480
   100  K  L  Y  C  Q  I  A  K  T  C  P  I  Q  I  K  V  S  T  P  P    119
   481  CCCCCGGGCACGGCCATCCGGGCCATGCCTGTCTACAAGAAGGCAGAGCATGTGACCGAC  540
   120  P  P  G  T  A  I  R  A  M  P  V  Y  K  K  A  E  H  V  T  D    139
   541  ATTGTTAAGCGCTGCCCCAACCACGAGCTTGGAAGGGACTTCAATGAAGGACAGTCTGCC  600
   140  I  V  K  R  C  P  N  H  E  L  G  R  D  F  N  E  G  Q  S  A    159
   601  CCGGCTAGCCACCTCATCCGTGTAGAAGGCAACAACCTCGCCCAGTACGTGGATGACCCT  660
   160  P  A  S  H  L  I  R  V  E  G  N  N  L  A  Q  Y  V  D  D  P    179
   661  GTCACCGGAAGGCAGAGTGTGGTTGTGCCGTATGAACCCCCACAGGTGGGAACAGAATTT  720
   180  V  T  G  R  Q  S  V  V  V  P  Y  E  P  P  Q  V  G  T  E  F    199
   721  ACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGTGTGGGGGGCATGAATCGGAGG  780
   200  T  T  I  L  Y  N  F  M  C  N  S  S  C  V  G  G  M  N  R  R    219
   781  CCCATCCTTGTCATCATCACCCTGGAGACCCGGGATGGACAGGTCCTGGGCCGCCGGTCT  840
   220  P  I  L  V  I  I  T  L  E  T  R  D  G  Q  V  L  G  R  R  S    239
   841  TTCGAGGGTCGCATCTGTGCCTGTCCTGGCCGTGACCGCAAAGCTGATGAAGACCATTAC  900
   240  F  E  G  R  I  C  A  C  P  G  R  D  R  K  A  D  E  D  H  Y    259
   901  CGGGAGCAACAGGCTCTGAATGAAAGTACCACCAAAAATGGAGCTGCCAGCAAACGTGCA  960
   260  R  E  Q  Q  A  L  N  E  S  T  T  K  N  G  A  A  S  K  R  A    279
   961  TTCAAGCAGAGCCCCCCTGCCATCCCTGCCCTGGGTACCAACGTGAAGAAGAGACGCCAC 1020
   280  F  K  Q  S  P  P  A  I  P  A  L  G  T  N  V  K  K  R  R  H    299
  1021  GGGGACGAGGACATGTTCTACATGCACGTGCGAGGCCGGGAGAACTTTGAGATCTTGATG 1080
   300  G  D  E  D  M  F  Y  M  H  V  R  G  R  E  N  F  E  I  L  M    319
  1081  AAAGTCAAGGAGAGCCTAGAACTGATGGAGCTTGTGCCCCAGCCTTTGGTTGACTCCTAT 1140
   320  K  V  K  E  S  L  E  L  M  E  L  V  P  Q  P  L  V  D  S  Y    339
  1141  CGACAGCAGCAGCAGCAGCTCCTACAGAGGCCGAGTCACCTGCAGCCTCCATCCTATT 1200
   340  R  Q  Q  Q  Q  Q  Q  L  L  Q  R  P  S  H  L  Q  P  P  S  Y    359
  1201  GGGCCCGTGCTCTCCCCAATGAACAAGGTACACGGTGGTGTCAACAAACTGCCCTCCGTC 1260
   360  G  P  V  L  S  P  M  N  K  V  H  G  G  V  N  K  L  P  S  V    379
  1261  AACCAGCTGGTGGGCCAGCCTCCCCCGCACAGCTCAGCAGCTGGGCCCAACCTGGGGCCC 1320
   380  N  Q  L  V  G  Q  P  P  P  H  S  S  A  A  G  P  N  L  G  P    399
  1321  ATGGGCTCCGGGATGCTCAACAGCCACGGCCACAGCATGCCGGCCAATGGTGAGATGAAT 1380
   400  M  G  S  G  M  L  N  S  H  G  H  S  M  P  A  N  G  E  M  N    419
  1381  GGAGGCCACAGCTCCCAGACCATGGTTTCGGGATCCCACTGCACCCCGCCACCCCCCTAT 1440
   420  G  G  H  S  S  Q  T  M  V  S  G  S  H  C  T  P  P  P  P  Y    439
  1441  CATGCAGACCCCAGCCTCGTCAGTTTTTTGACAGGGTTGGGGTGTCCAAACTGCATCGAG 1500
   440  H  A  D  P  S  L  V  S  F  L  T  G  L  G  C  P  N  C  I  E    459
  1501  TGCTTCACTTCCCAAGGGTTGCAGAGCATCTACCACCTGCAGAACCTTACCATCGAGGAC 1560
   460  C  F  T  S  Q  G  L  Q  S  I  Y  H  L  Q  N  L  T  I  E  D    479
  1561  CTTGGGGCTCTGAAGGTCCCTGACCAGTACCGTATGACCATCTGGAGGGGCCTACAGGAC 1620
   480  L  G  A  L  K  V  P  D  Q  Y  R  M  T  I  W  R  G  L  Q  D    499
  1621  CTGAAGCAGAGCCATGACTGCGGCCAGCAACTGCTACGCTCCAGCAGCAACGCGGCCACC 1680
   500  L  K  Q  S  H  D  C  G  Q  Q  L  L  R  S  S  S  N  A  A  T    519
  1681  ATCTCCATCGGCGGCTCTGGCGAGCTGCAGCGGCAGCGGGTCATGGAAGCCGTGCATTTC 1740
   520  I  S  I  G  G  S  G  E  L  Q  R  Q  R  V  M  E  A  V  H  F    539
  1741  CGTGTGCGCCACACCATCACAATCCCCAACCGTGGAGGCGCAGGTGCGGTGACAGGTCCC 1800
   540  R  V  R  H  T  I  T  I  P  N  R  G  G  A  G  A  V  T  G  P    559
  1801  GACGAGTGGGCGGACTTTGGCTTTGACCTGCCTGACTGCAAGTCCCGTAAGCAGCCCATC 1860
   560  D  E  W  A  D  F  G  F  D  L  P  D  C  K  S  R  K  Q  P  I    579
  1861  AAAGAGGAGTTCACAGAGACAGAGAGCCACTGAGGAACGTACCTTCTTCTCCTGTCCTTC 1920
   580  K  E  E  F  T  E  T  E  S  H  *                              599
  1921  CTCTGTGAGAAACTGCTCTTGGAAGTGGGACCTGTTGGCTGTGCCCACAGAAACCAGCAA 1980
  1981  GGACCTTCTGCCGGATGCCATTCCTGAAGGGAAGTCGCTCATGAACTAACTCCCTCTTGG 2040
```

FIG.7

```
     1  TGGTCCCGCTTCGACCAAGACTCCGGCTACCAGCTTGCGGGCCCCGCGGAGGAGGAGACC   60
    61  CCGCTGGGGCTAGCTGGGCGACGCGCGCCAAGCGGCGGCGGGAAGGAGGCGGGAGGAGCG  120
   121  GGGCCCGAGACCCCGACTCGGGCAGAGCCAGCTGGGGAGGCGGGGCGCGCGTGGGAGCCA  180
   181  GGGGCCCGGGTGGCCGGCCCTCCTCCGCCACGGCTGAGTGCCCGCGCTGCCTTCCCGCCG  240
   241  GTCCGCCAAGAAAGGCGCTAAGCCTGCGGCAGTCCCCTCGCCGCCGCCTCCCTGCTCCGC  300
   301  ACCCTTATAACCCGCCGTCCCGCATCCAGGCGAGGAGGCAACGCTGCAGCCCAGCCCTCG  360
   361  CCGACGCCGACGCCCGGCCCGGAGCAGAATGAGCGGCAGCGTTGGGGAGATGGCCCAGAC  420
    -8                                  M  S  G  S  V  G  E  M  A  Q  T   11
   421  CTCTTCTTCCTCCTCCTCCACCTTCGAGCACCTGTGGAGTTCTCTAGAGCCAGACAGCAC  480
    12   S  S  S  S  S  S  T  F  E  H  L  W  S  S  L  E  P  D  S  T   31
   481  CTACTTTGACCTCCCCCAGCCCAGCCAAGGGACTAGCGAGGCATCAGGCAGCGAGGAGTC  540
    32   Y  F  D  L  P  Q  P  S  Q  G  T  S  E  A  S  G  S  E  E  S   51
   541  CAACATGGATGTCTTCCACCTGCAAGGCATGGCCCAGTTCAATTTGCTCAGCAGTGCCAT  600
    52   N  M  D  V  F  H  L  Q  G  M  A  Q  F  N  L  L  S  S  A  M   71
   601  GGACCAGATGGGCAGCCGTGCGGCCCCGGCGAGCCCCTACACCCCGGAGCACGCCGCCAG  660
    72   D  Q  M  G  S  R  A  A  P  A  S  P  Y  T  P  E  H  A  A  S   91
   661  CGCGCCCACCCACTCGCCCTACGCGCAGCCCAGCTCCACCTTCGACACCATGTCTCCGGC  720
    92   A  P  T  H  S  P  Y  A  Q  P  S  S  T  F  D  T  M  S  P  A  111
   721  GCCTGTCATCCCTTCCAATACCGACTACCCCGGCCCCC  758
   112   P  V  I  P  S  N  T  D  Y  P  G  P    123
```

FIG. 8

```
_ Name: sr-p70a-cos3      Len:    650  Check: 9661  Weight:  1.00
_ Name: sr-p70b-cos3      Len:    650  Check: 3605  Weight:  1.00
_ Name: sr-p70-ht29       Len:    650  Check:   85  Weight:  1.00
_ Name: sr-p70c-att20     Len:    650  Check: 4072  Weight:  1.00
_ Name: sr-p70a-att20     Len:    650  Check: 4204  Weight:  1.00
_
_//
_
_                  1                                            50
_ sr-p70a-cos3     .......MAQ STTTSPDGGT TFEHLWSSLE PDSTYFDLPQ SSRGNNEVVG
_ sr-p70b-cos3     .......MAQ STTTSPDGGT TFEHLWSSLE PDSTYFDLPQ SSRGNNEVVG
_  sr-p70-ht29     .......MAQ STATSPDGGT TFEHLWSSLE PDSTYFDLPQ SSRGNNEVVG
_sr-p70c-att20     .......... .......... .......... .......... ..........
_sr-p70a-att20     MSGSVGEMAQ ...TSSSSSS TFEHLWSSLE PDSTYFDLPQ PSQGTSEASG
_
_                  51                                           100
_ sr-p70a-cos3     GTDSSMD.VF HLEGMTTSVM AQFNLLSSTM DQMSSRAASA SPYTPEHAAS
_ sr-p70b-cos3     GTDSSMD.VF HLEGMTTSVM AQFNLLSSTM DQMSSRAASA SPYTPEHAAS
_  sr-p70-ht29     GTDSSMD.VF HLEGMTTSVM AQFNLLSSTM DQMSSRAASA SPYTPEHAAS
_sr-p70c-att20     ...MCMGPVY ..ESLG...Q AQFNLLSSAM DQMGSRAAPA SPYTPEHAAS
_sr-p70a-att20     SEESNMD.VF HLQGM..... AQFNLLSSAM DQMGSRAAPA SPYTPEHAAS
_
_                  101                                          150
_ sr-p70a-cos3     VPTHSPYAQP SSTFDTMSPA PVIPSNTDYP GPHHFEVTFQ QSSTAKSATW
_ sr-p70b-cos3     VPTHSPYAQP SSTFDTMSPA PVIPSNTDYP GPHHFEVTFQ QSSTAKSATW
_  sr-p70-ht29     VPTHSPYAQP SSTFDTMSPA PVIPSNTDYP GPHHFEVTFQ QSSTAKSATW
_sr-p70c-att20     APTHSPYAQP SSTFDTMSPA PVIPSNTDYP GPHHFEVTFQ QSSTAKSATW
_sr-p70a-att20     APTHSPYAQP SSTFDTMSPA PVIPSNTDYP GP........ ..........
_
_                  151                                          200
_ sr-p70a-cos3     TYSPLLKKLY CQIAKTCPIQ IKVSAPPPPG TAIRAMPVYK KAEHVTDIVK
_ sr-p70b-cos3     TYSPLLKKLY CQIAKTCPIQ IKVSAPPPPG TAIRAMPVYK KAEHVTDIVK
_  sr-p70-ht29     TYSPLLKKLY CQIAKTCPIQ IKVSTPPPPG TAIRAMPVYK KAEHVTDVVK
_sr-p70c-att20     TYSPLLKKLY CQIAKTCPIQ IKVSTPPPPG TAIRAMPVYK KAEHVTDIVK
_sr-p70a-att20     .......... .......... .......... .......... ..........
_
_                  201                                          250
_ sr-p70a-cos3     RCPNHELGRD FNEGQSAPAS HLIRVEGNNL SQYVDDPVTG RQSVVVPYEP
_ sr-p70b-cos3     RCPNHELGRD FNEGQSAPAS HLIRVEGNNL SQYVDDPVTG RQSVVVPYEP
_  sr-p70-ht29     RCPNHELGRD FNEGQSAPAS HLIRVEGNNL SQYVDDPVTG RQSVVVPYEP
_sr-p70c-att20     RCPNHELGRD FNEGQSAPAS HLIRVEGNNL AQYVDDPVTG RQSVVVPYEP
_sr-p70a-att20     .......... .......... .......... .......... ..........
_
_                  251                                          300
_ sr-p70a-cos3     PQVGTEFTTI LYNFMCNSSC VGGMNRRPIL IIITLETRDG QVLGRRSFEG
_ sr-p70b-cos3     PQVGTEFTTI LYNFMCNSSC VGGMNRRPIL IIITLETRDG QVLGRRSFEG
_  sr-p70-ht29     PQVGTEFTTI LYNFMCNSSC VGGMNRRPIL IIITLEMRDG QVLGRRSFEG
_sr-p70c-att20     PQVGTEFTTI LYNFMCNSSC VGGMNRRPIL VIITLETRDG QVLGRRSFEG
_sr-p70a-att20     .......... .......... .......... .......... ..........
_
_                  301                                          350
_ sr-p70a-cos3     RICACPGRDR KADEDHYREQ QALNESSAKN GAASKRAFKQ SPPAVPALGP
_ sr-p70b-cos3     RICACPGRDR KADEDHYREQ QALNESSAKN GAASKRAFKQ SPPAVPALGP
_  sr-p70-ht29     RICACPGRDR KADEDHYREQ QALNESSAKN GAASKRAFKQ SPPAVPALGA
_sr-p70c-att20     RICACPGRDR KADEDHYREQ QALNESTTKN GAASKRAFKQ SPPAIPALGT
_sr-p70a-att20     .......... .......... .......... .......... ..........
_
```

FIG.9

```
                351                                                     400
_ sr-p70a-cos3  GVKKRRHGDE DTYYLQVRGR ENFEILMKLK ESLELMELVP QPLVDSYR..
_ sr-p70b-cos3  GVKKRRHGDE DTYYLQVRGR ENFEILMKLK ESLELMELVP QPLVDSYR..
_  sr-p70-ht29  GVKKRRHGDE DTYYLQVRGR ENFEILMKLK ESLELMELVP QPLVDSYR..
_sr-p70c-att20  NVKKRRHGDE DMFYMHVRGR ENFEILMKVK ESLELMELVP QPLVDSYRQQ
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
                401                                                     450
_ sr-p70a-cos3  QQQQLLQRPS HLQPPSYGPV LSPMNKVHGG VNKLPSVNQL VGQPPPHSSA
_ sr-p70b-cos3  QQQQLLQRPS HLQPPSYGPV LSPMNKVHGG VNKLPSVNQL VGQPPPHSSA
_  sr-p70-ht29  QQQQLLQRPS HLQPPSYGPV LSPMNKVHGG MNKLPSVNQL VGQPPPHSSA
_sr-p70c-att20  QQQQLLQRPS HLQPPSYGPV LSPMNKVHGG VNKLPSVNQL VGQPPPHSSA
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
                451                                                     500
_ sr-p70a-cos3  ATPNLGPVGS GMLNNHGHAV PANSEMTSSH GTQSMVSGSH CTPPPPYHAD
_ sr-p70b-cos3  ATPNLGPVGS GMLNNHGHAV PANSEMTSSH GTQSMVSGSH CTPPPPYHAD
_  sr-p70-ht29  ATPNLGPVGP GMLNNHGHAV PANGEMSSSH SAQSMVSGSH CTPPPPYHAD
_sr-p70c-att20  AGPNLGPMGS GMLNSHGHSM PANGEMNGGH SSQTMVSGSH CTPPPPYHAD
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
                501                                                     550
_ sr-p70a-cos3  PSLVSFLTGL GCPNCIEYFT SQGLQSIYHL QNLTIEDLGA LKIPEQYRMT
_ sr-p70b-cos3  PSLVR..T.W G.P..... .......... .......... ..........
_  sr-p70-ht29  PSLVSFLTGL GCPNCIEYFT SQGLQSIYHL QNLTIEDLGA LKIPEQYRMT
_sr-p70c-att20  PSLVSFLTGL GCPNCIECFT SQGLQSIYHL QNLTIEDLGA LKVPDQYRMT
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
                551                                                     600
_ sr-p70a-cos3  IWRGLQDLKQ GHDYGAAAQQ LLR.SSNAAA ISIGGSGELQ RQRVMEAVHF
_ sr-p70b-cos3  .......... .......... .......... .......... ..........
_  sr-p70-ht29  IWRGLQDLKQ GHDYS.TAQQ LLR.SSNAAT ISIGGSGELQ RQRVMEAVHF
_sr-p70c-att20  IWRGLQDLKQ SHDCG...QQ LLRSSSNAAT ISIGGSGELQ RQRVMEAVHF
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
                601                                                     650
_ sr-p70a-cos3  RVRHTITIPN RGGPGA..GP DEWADFGFDL PDCKARKQPI KEEFTEAEIH
_ sr-p70b-cos3  .......... .......... .......... .......... ..........
_  sr-p70-ht29  RVRHTITIPN RGGPGG..GP DEWADFGFDL PDCKARKQPI KEEFTEAEIH
_sr-p70c-att20  RVRHTITIPN RGGAGAVTGP DEWADFGFDL PDCKSRKQPI KEEFTETESH
_sr-p70a-att20  .......... .......... .......... .......... ..........
_
_
```

FIG.9 cont.

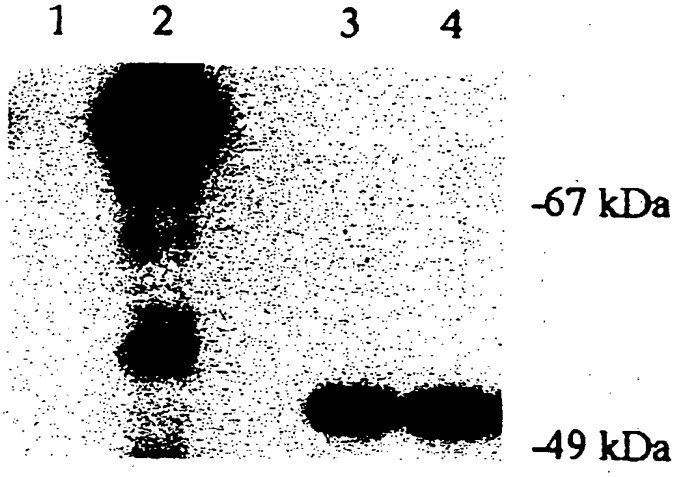


FIG.10a

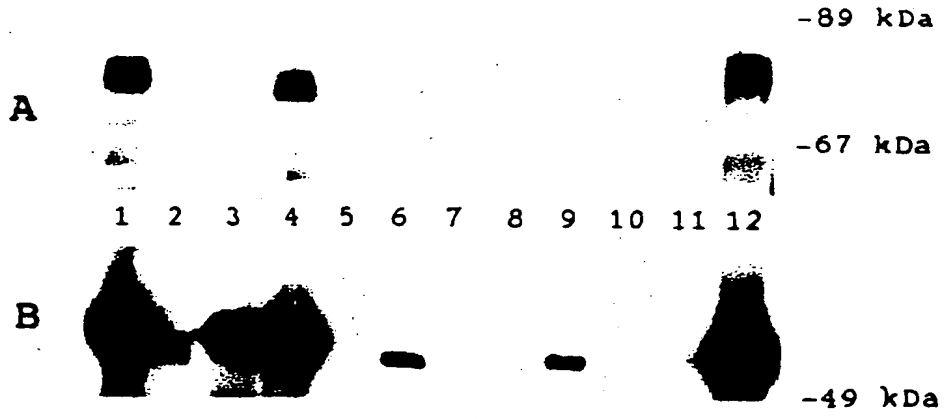


FIG.10b

FIG.11

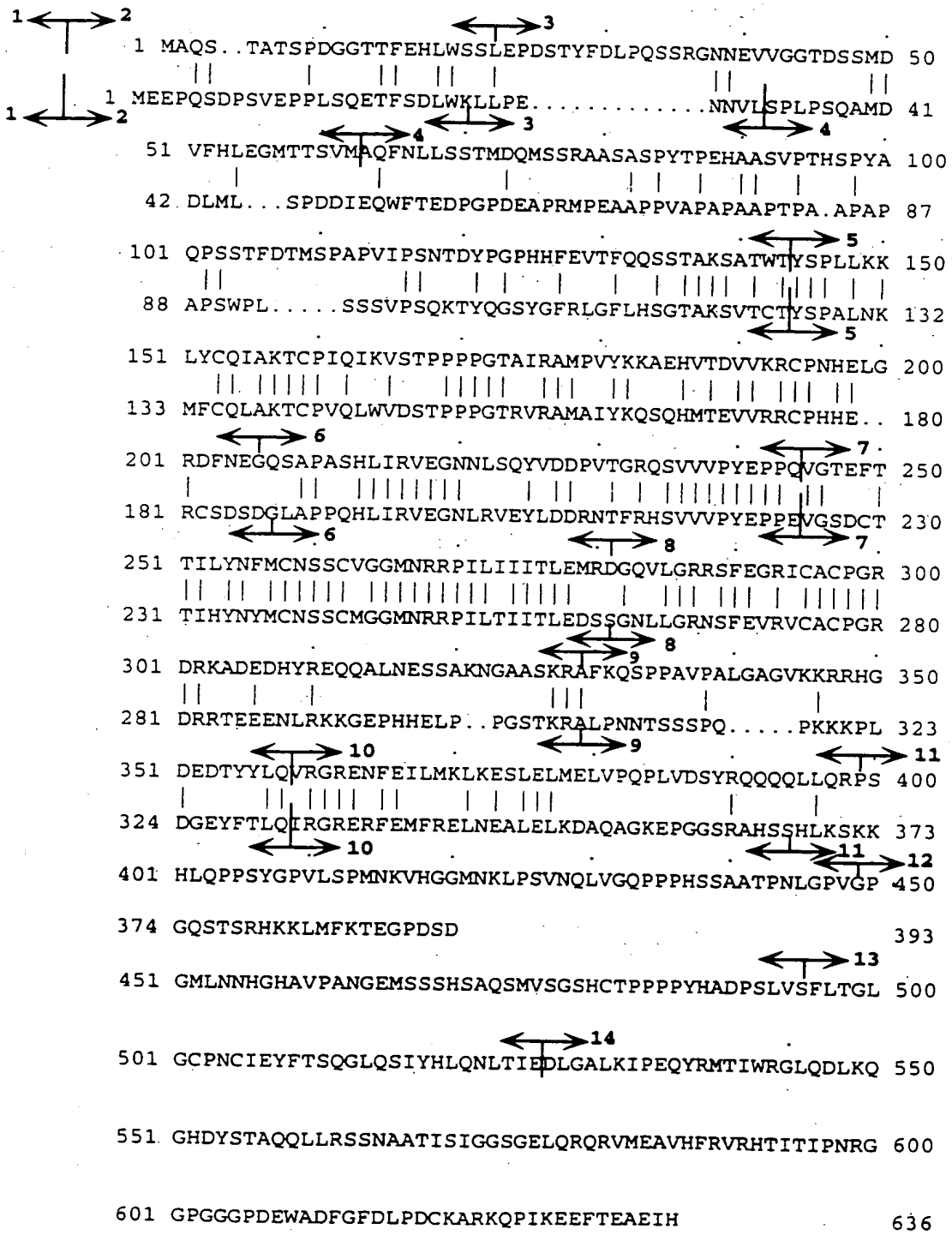

1 MAQS..TATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGGTDSSMD 50
1 MEEPQSDPSVEPPLSQETFSDLWKLLPE.....NNVLSPLPSQAMD 41
51 VFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 100
42 DLML...SPDDIEQWFTEDPGPDEAPRMPEAAPPVAPAPAAPTPA.APAP 87
101 QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 150
88 APSWPL.....SSSVPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNK 132
151 LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 200
133 MFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHE.. 180
201 RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 250
181 RCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCT 230
251 TILYNFMCNSSCVGGMNRRPILIIITLEMRDGQVLGRRSFEGRICACPGR 300
231 TIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGR 280
301 DRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHG 350
281 DRRTEEENLRKKGEPHHELP..PGSTKRALPNNTSSSPQ.....PKKKPL 323
351 DEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPS 400
324 DGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPGGSRAHSSHLKSKK 373
401 HLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGP 450
374 GQSTSRHKKLMFKTEGPDSD 393
451 GMLNNHGHAVPANGEMSSSHSAQSMVSGSHCTPPPPYHADPSLVSFLTGL 500
501 GCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQ 550
551 GHDYSTAQQLLRSSNAATISIGGSGELQRQRVMEAVHFRVRHTITIPNRG 600
601 GPGGGPDEWADFGFDLPDCKARKQPIKEEFTEAEIH 636

FIG.12

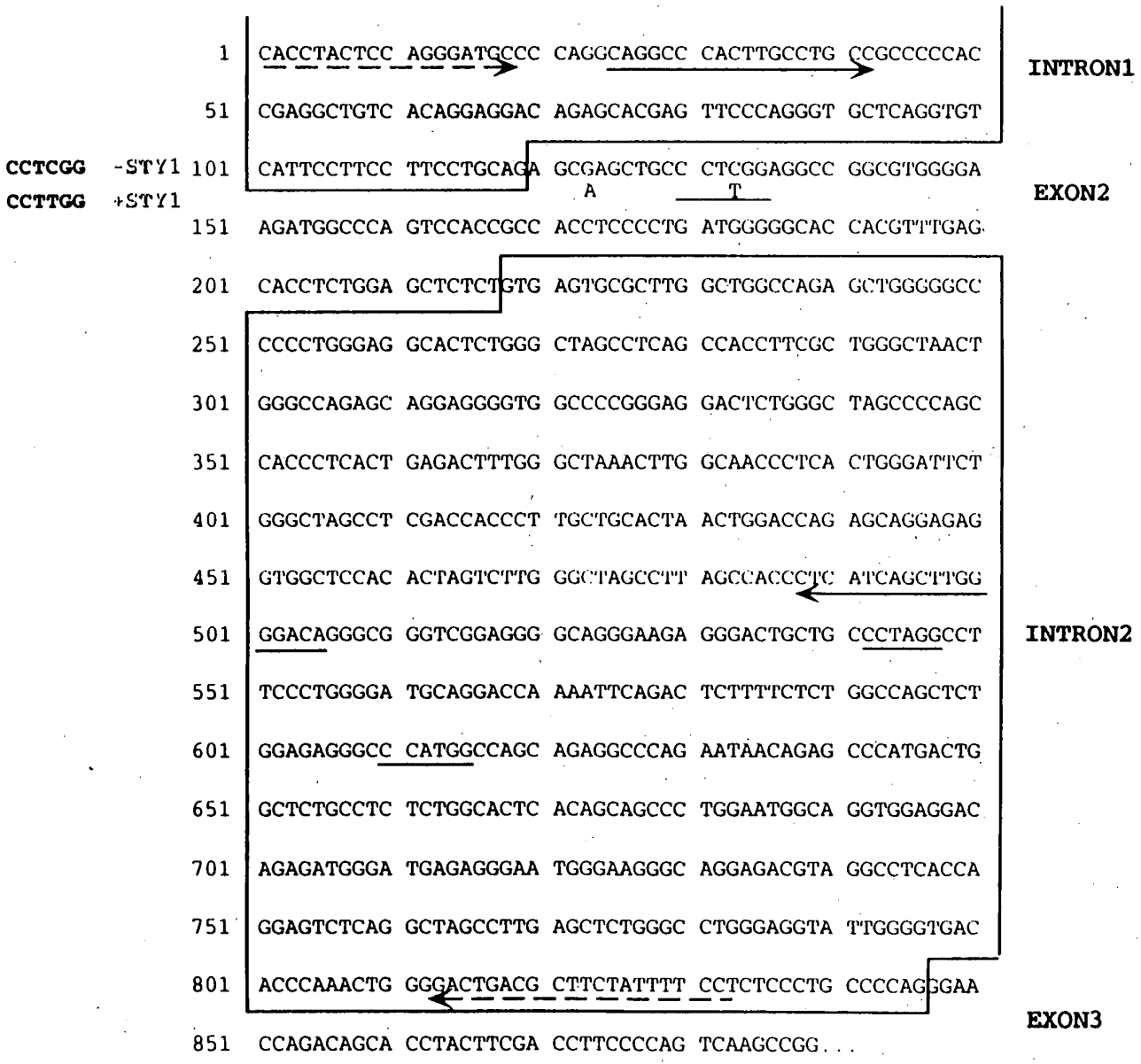

1 CACCTACTCC AGGGATGCCC CAGGCAGGCC CACTTGCCTG CCGCCCCCAC
INTRON1
51 CGAGGCTGTC ACAGGAGGAC AGAGCACGAG TTCCCAGGGT GCTCAGGTGT
CCTCGG -STY1 101 CATTCCTTCC TTCCTGCAGA GCGAGCTGCC CTCGGAGGCC GGCGTGGGGA
CCTTGG +STY1
A T
EXON2
151 AGATGGCCCA GTCCACCGCC ACCTCCCCTG ATGGGGGCAC CACGTTTGAG
201 CACCTCTGGA GCTCTCTGTG AGTGCGCTTG GCTGGCCAGA GCTGGGGGCC
251 CCCCTGGGAG GCACTCTGGG CTAGCCTCAG CCACCTTCGC TGGGCTAACT
301 GGGCCAGAGC AGGAGGGGTG GCCCCGGGAG GACTCTGGGC TAGCCCCAGC
351 CACCCTCACT GAGACTTTGG GCTAAACTTG GCAACCCTCA CTGGGATTCT
401 GGGCTAGCCT CGACCACCCT TGCTGCACTA ACTGGACCAG AGCAGGAGAG
451 GTGGCTCCAC ACTAGTCTTG GGCTAGCCTT AGCCACCCTC ATCAGCTTGG
501 GGACAGGGCG GGTCGGAGGG GCAGGGAAGA GGGACTGCTG CCCTAGGCCT
INTRON2
551 TCCCTGGGGA TGCAGGACCA AAATTCAGAC TCTTTTCTCT GGCCAGCTCT
601 GGAGAGGGCC CATGGCCAGC AGAGGCCCAG AATAACAGAG CCCATGACTG
651 GCTCTGCCTC TCTGGCACTC ACAGCAGCCC TGGAATGGCA GGTGGAGGAC
701 AGAGATGGGA TGAGAGGGAA TGGGAAGGGC AGGAGACGTA GGCCTCACCA
751 GGAGTCTCAG GCTAGCCTTG AGCTCTGGGC CTGGGAGGTA TTGGGGTGAC
801 ACCCAAACTG GGGACTGACG CTTCTATTTT CCTCTCCCTG CCCCAGGGAA
EXON3
851 CCAGACAGCA CCTACTTCGA CCTTCCCCAG TCAAGCCGG...

FIG.13

```
sr-p70d-imr32                                  CG ACCTTCCCCA GTCAAGCCGG GGGAATAATG 32
sr-p70a-ht29                                   CG ACCTTCCCCA GTCAAGCCGG GGGAATAATG 150

AGGTGGTGGG CGGAACGGAT TCCAGCATGG ACGTCTTCCA CCTGGAGGGC 82
AGGTGGTGGG CGGAACGGAT TCCAGCATGG ACGTCTTCCA CCTGGAGGGC 200

ATGACTACAT CTGTCATGCA TCCTCGGCTC CTGCCTCACT AGCTGCGGAG 132
ATGACTACAT CTGTCAT... .......... .......... .......... 217

CCTCTCCCGC TCGGTCCACG CTGCCGGGCG GCCACGACCG TGACCCTTCC 182
.......... .......... .......... .......... ..........

CCTCGGGCCG CCCAGATCCA TGCCTCGTCC CACGGGACAC CAGTTCCCTG 232
.......... .......... .......... .......... ..........

GCGTGTGCAG ACCCCCCGGC GCCTACCATG CTGTACGTCG GTGACCCCGC 282
.......... .......... .......... .......... ..........

ACGGCACCTC GCCACGGCCC AGTTCAATCT GCTGAGCAGC ACCATGGACC 332
.......... .....GGCCC AGTTCAATCT GCTGAGCAGC ACCATGGACC 252

AGATGAGCAG CCGCGCGGCC TCGGCCAGCC CCTACACCCC AGAGCACGCC 382
AGATGAGCAG CCGCGCGGCC TCGGCCAGCC CCTACACCCC AGAGCACGCC 302

GCCAGCGTGC CCACCCACTC GCCCTACGCA CAACCCAGCT CCACCTTCGA 432
GCCAGCGTGC CCACCCAcTC GCCCTACGCA CAACCCAGCT CCACCTTCGA 352

CACCATGTCG CCGGCGCCTG TCATCCCCTC CAACACCGAC TACCCCGGAC 482
CACCATGTCG CCGGCGCCTG TCATCCCCTC CAACACCGAC TACCCCGGAC 402

CCCACCACTT TGAGGTCACT TTCCAGCAGT CCAGCACGGC CAAGTCAGCC 532
CCCACCACTT TGAGGTCACT TTCCAGCAGT CCAGCACGGC CAAGTCAGCC 452

ACCTGGACGT ACTCCCCGCT CTTGAAG
ACCTGGACGT ACTCCCCGCT CTTGAAG
```

FIG. 14

```
sr-p70a TAACGCCCGCGGCCGCCTACTCCCCGCGGCGCCTCCCCTCCCCGCGCCCA   50
sr-p70f ----------------------------------------------------   0
sr-p70d ----------------------------------------------------   0
sr-p70e ----------------------------------------------------   0
sr-p70b ----------------------------------------------------   0

sr-p70a TATAACCCGCCTAGGGGCCGGGCAGCCCGCCCTGCCTCCCCGCCCGCGCA  100
sr-p70f ----------------------------------------------------   0
sr-p70d ----------------------------------------------------   0
sr-p70e ----------------------------------------------------   0
sr-p70b ----------------------------------------------------   0

sr-p70a CCCGCCCGGAGGCTCGCGCGCCCGCGAAGGGGACGCAGCGAAACCGGGGC  150
sr-p70f ----------------------------------------------------   0
sr-p70d ----------------------------------------------------   0
sr-p70e ----------------------------------------------------   0
sr-p70b ----------------------------------------------------   0

sr-p70a CCGCGCCAGGCCAGCCGGGACGGACGCCGATGCCCGGGGCTGCGACGGCT  200
sr-p70f ----------------------------TGCCCGGGGCTGCGACGGCT   20
sr-p70d ----------------------------------------------------   0
sr-p70e ----------------------------------------------------   0
sr-p70b ----------------------------------------------------   0

sr-p70a GCAGAGCGAGCTGCCCTCGGAGGCCGGCGTGGGGAAGATGGCCCAGTCCA  250
sr-p70f GCAG------------------------------------------------   24
sr-p70d ----------------------------------------------------   0
sr-p70e ----------------------------------------------------   0
sr-p70b ----------------------------------------ATGGCCCAGTCCA   13
```

FIG. 15

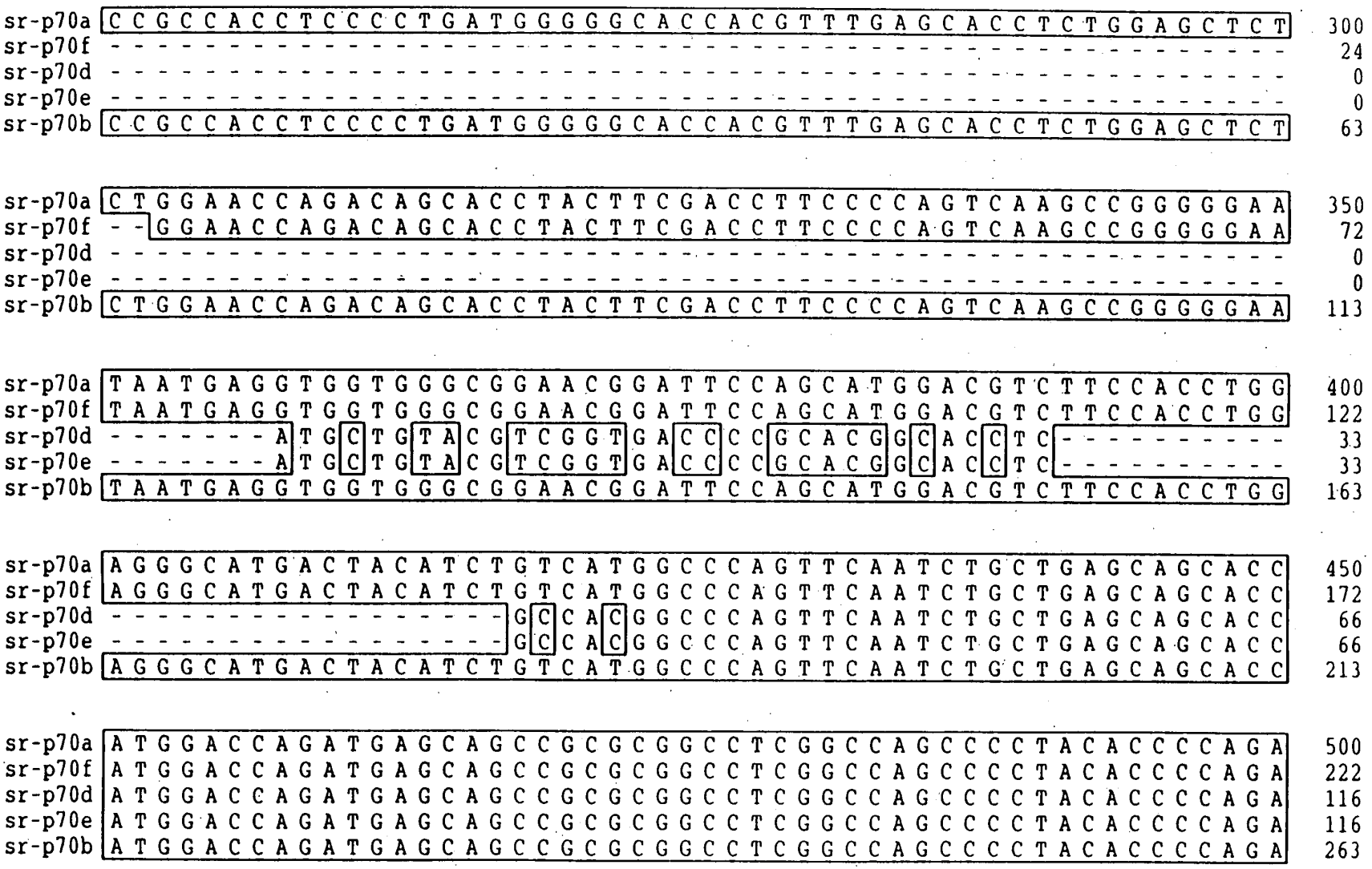

sr-p70a CCGCCACCTCCCCTGATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCT 300
sr-p70f -- 24
sr-p70d -- 0
sr-p70e -- 0
sr-p70b CCGCCACCTCCCCTGATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCT 63
sr-p70a CTGGAACCAGACAGCACCTACTTCGACCTTCCCCAGTCAAGCCGGGGGAA 350
sr-p70f --GGAACCAGACAGCACCTACTTCGACCTTCCCCAGTCAAGCCGGGGGAA 72
sr-p70d -- 0
sr-p70e -- 0
sr-p70b CTGGAACCAGACAGCACCTACTTCGACCTTCCCCAGTCAAGCCGGGGGAA 113
sr-p70a TAATGAGGTGGTGGGCGGAACGGATTCCAGCATGGACGTCTTCCACCTGG 400
sr-p70f TAATGAGGTGGTGGGCGGAACGGATTCCAGCATGGACGTCTTCCACCTGG 122
sr-p70d --------ATGCTGTACGTCGGTGACCCCGCACGGCACTC---------- 33
sr-p70e --------ATGCTGTACGTCGGTGACCCCGCACGGCACTC---------- 33
sr-p70b TAATGAGGTGGTGGGCGGAACGGATTCCAGCATGGACGTCTTCCACCTGG 163
sr-p70a AGGGCATGACTACATCTGTCATGGCCCAGTTCAATCTGCTGAGCAGCACC 450
sr-p70f AGGGCATGACTACATCTGTCATGGCCCAGTTCAATCTGCTGAGCAGCACC 172
sr-p70d ----------------GCCACGGCCCAGTTCAATCTGCTGAGCAGCACC 66
sr-p70e ----------------GCCACGGCCCAGTTCAATCTGCTGAGCAGCACC 66
sr-p70b AGGGCATGACTACATCTGTCATGGCCCAGTTCAATCTGCTGAGCAGCACC 213
sr-p70a ATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGA 500
sr-p70f ATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGA 222
sr-p70d ATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGA 116
sr-p70e ATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGA 116
sr-p70b ATGGACCAGATGAGCAGCCGCGCGGCCTCGGCCAGCCCCTACACCCCAGA 263

FIG.15 cont.

```
sr-p70a GCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCA 550
sr-p70f GCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCA 272
sr-p70d GCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCA 166
sr-p70e GCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCA 166
sr-p70b GCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAACCCAGCTCCA 313

sr-p70a CCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC 600
sr-p70f CCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC 322
sr-p70d CCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC 216
sr-p70e CCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC 216
sr-p70b CCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC 363

sr-p70a CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAA 650
sr-p70f CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAA 372
sr-p70d CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAA 266
sr-p70e CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAA 266
sr-p70b CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAA 413

sr-p70a GTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGA 700
sr-p70f GTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGA 422
sr-p70d GTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGA 316
sr-p70e GTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGA 316
sr-p70b GTCAGCCACCTGGACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGA 463

sr-p70a TCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCACCCCCA 750
sr-p70f TCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCACCCCCA 472
sr-p70d TCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCACCCCCA 366
sr-p70e TCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCACCCCCA 366
sr-p70b TCGCCAAGACATGCCCCATCCAGATCAAGGTGTCCACCCCGCCACCCCCA 513
```

FIG.15 cont.

```
sr-p70a GGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGAC  800
sr-p70f GGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGAC  522
sr-p70d GGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGAC  416
sr-p70e GGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGAC  416
sr-p70b GGCACTGCCATCCGGGCCATGCCTGTTTACAAGAAAGCGGAGCACGTGAC  563

sr-p70a CGACGTCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACG  850
sr-p70f CGACGTCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACG  572
sr-p70d CGACGTCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACG  466
sr-p70e CGACGTCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACG  466
sr-p70b CGACGTCGTGAAACGCTGCCCCAACCACGAGCTCGGGAGGGACTTCAACG  613

sr-p70a AAGGACAGTCTGCTCCAGCCAGCCACCTCATCCGCGTGGAAGGCAATAAT  900
sr-p70f AAGGACAGTCTGCTCCAGCCAGCCACCTCATCCGCGTGGAAGGCAATAAT  622
sr-p70d AAGGACAGTCTGCTCCAGCCAGCCACCTCATCCGCGTGGAAGGCAATAAT  516
sr-p70e AAGGACAGTCTGCTCCAGCCAGCCACCTCATCCGCGTGGAAGGCAATAAT  516
sr-p70b AAGGACAGTCTGCTCCAGCCAGCCACCTCATCCGCGTGGAAGGCAATAAT  663

sr-p70a CTCTCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGT  950
sr-p70f CTCTCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGT  672
sr-p70d CTCTCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGT  566
sr-p70e CTCTCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGT  566
sr-p70b CTCTCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGT  713

sr-p70a GCCCTATGAGCCACCACAGGTGGGGACGGAATTCACCACCATCCTGTACA 1000
sr-p70f GCCCTATGAGCCACCACAGGTGGGGACGGAATTCACCACCATCCTGTACA  722
sr-p70d GCCCTATGAGCCACCACAGGTGGGGACGGAATTCACCACCATCCTGTACA  616
sr-p70e GCCCTATGAGCCACCACAGGTGGGGACGGAATTCACCACCATCCTGTACA  616
sr-p70b GCCCTATGAGCCACCACAGGTGGGGACGGAATTCACCACCATCCTGTACA  763
```

FIG.15 cont.

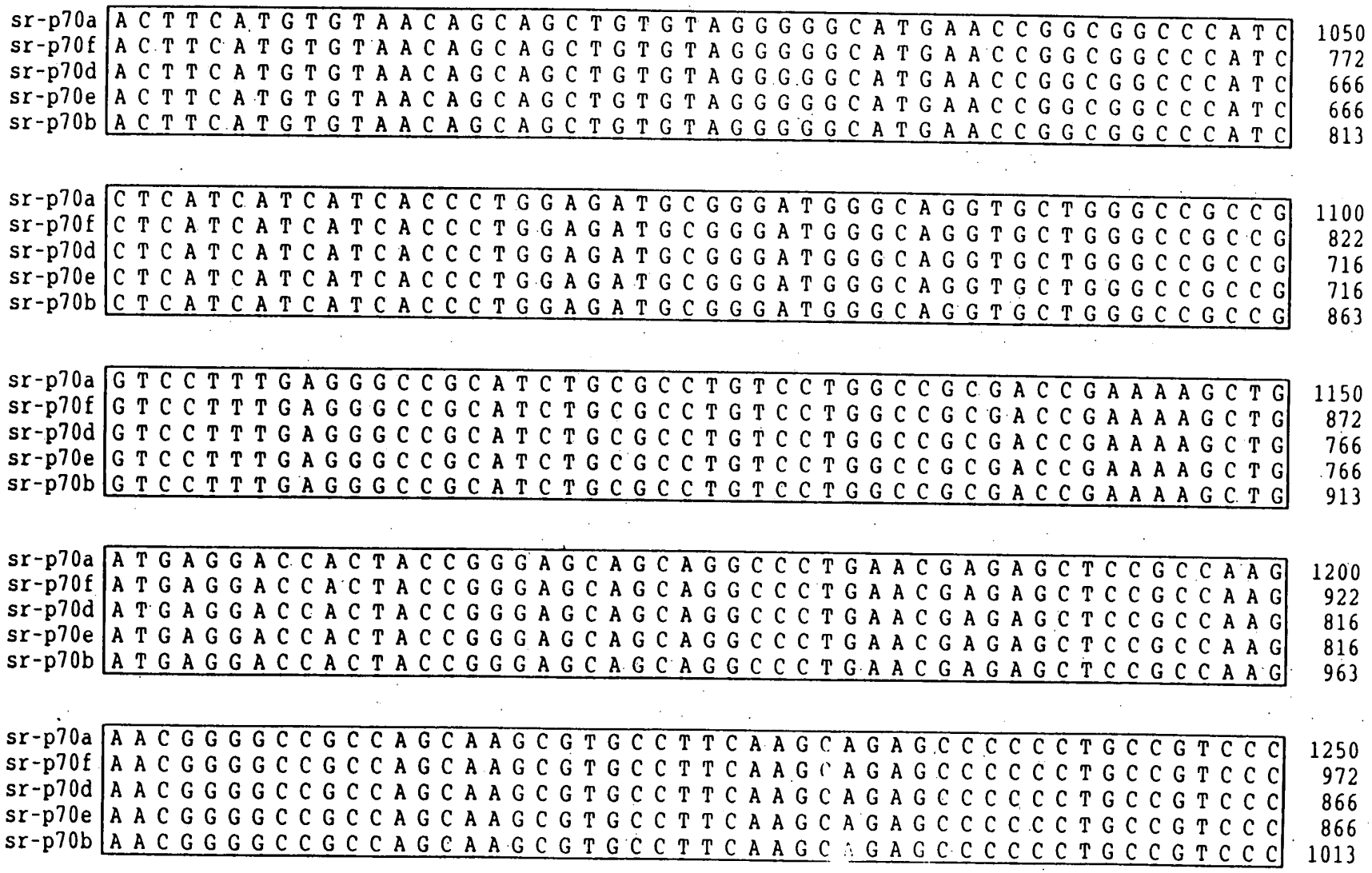
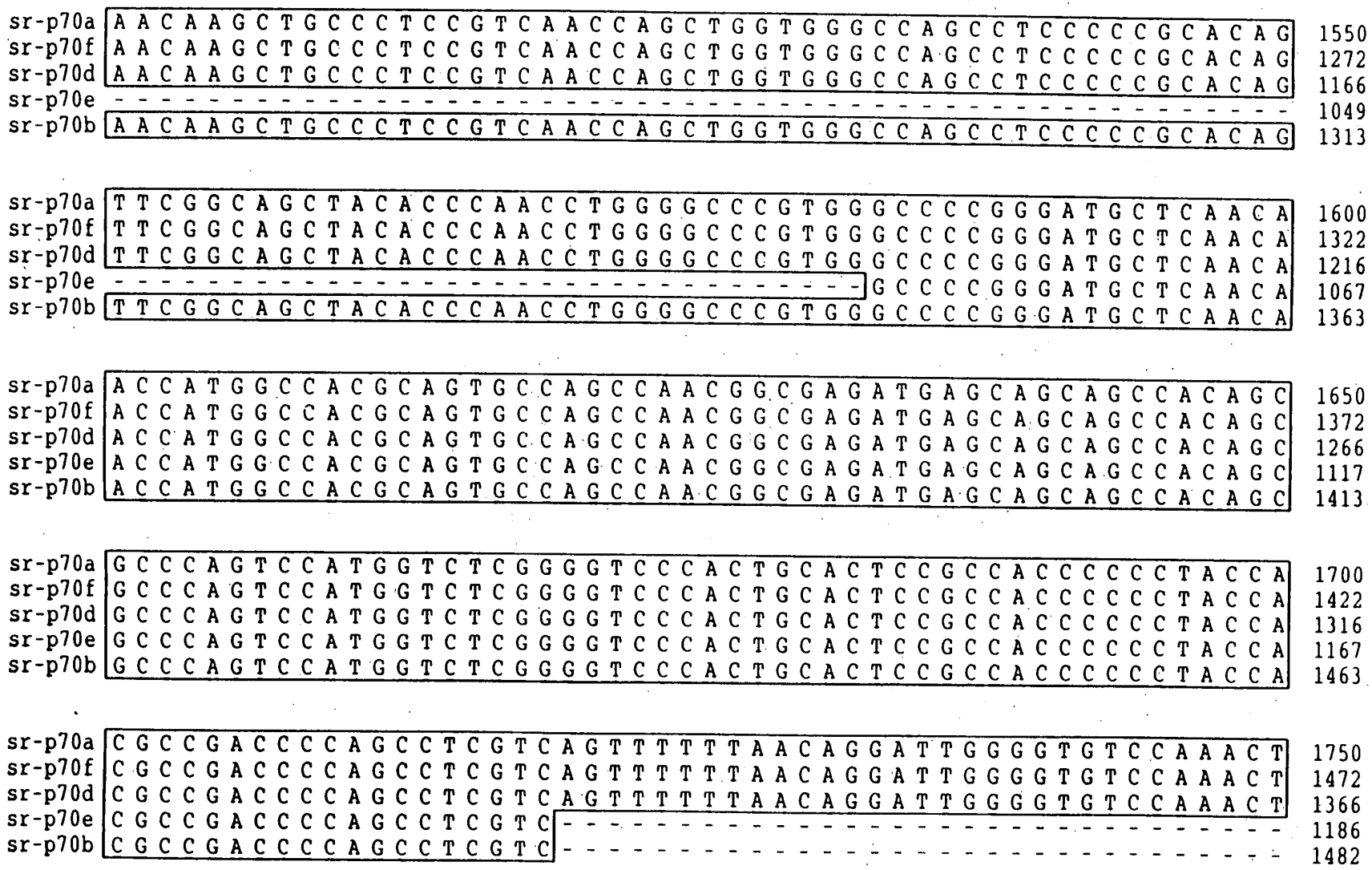

sr-p70a ACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGCCCATC 1050
sr-p70f ACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGCCCATC 772
sr-p70d ACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGCCCATC 666
sr-p70e ACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGCCCATC 666
sr-p70b ACTTCATGTGTAACAGCAGCTGTGTAGGGGGCATGAACCGGCGGCCCATC 813
sr-p70a CTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCG 1100
sr-p70f CTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCG 822
sr-p70d CTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCG 716
sr-p70e CTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCG 716
sr-p70b CTCATCATCATCACCCTGGAGATGCGGGATGGGCAGGTGCTGGGCCGCCG 863
sr-p70a GTCCTTTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTG 1150
sr-p70f GTCCTTTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTG 872
sr-p70d GTCCTTTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTG 766
sr-p70e GTCCTTTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTG 766
sr-p70b GTCCTTTGAGGGCCGCATCTGCGCCTGTCCTGGCCGCGACCGAAAAGCTG 913
sr-p70a ATGAGGACCACTACCGGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAG 1200
sr-p70f ATGAGGACCACTACCGGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAG 922
sr-p70d ATGAGGACCACTACCGGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAG 816
sr-p70e ATGAGGACCACTACCGGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAG 816
sr-p70b ATGAGGACCACTACCGGGAGCAGCAGGCCCTGAACGAGAGCTCCGCCAAG 963
sr-p70a AACGGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCC 1250
sr-p70f AACGGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCC 972
sr-p70d AACGGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCC 866
sr-p70e AACGGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCC 866
sr-p70b AACGGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCC 1013

FIG. 15 cont.

```
sr-p70a C G C C C T T G G T G C C G G T G T G A A G A A G C G G C G G C A T G G A G A C G A G G A C A C G T  1300
sr-p70f C G C C C T T G G T G C C G G T G T G A A G A A G C G G C G G C A T G G A G A C G A G G A C A C G T  1022
sr-p70d C G C C C T T G G T G C C G G T G T G A A G A A G C G G C G G C A T G G A G A C G A G G A C A C G T   916
sr-p70e C G C C C T T G G T G C C G G T G T G A A G A A G C G G C G G C A T G G A G A C G A G G A C A C G T   916
sr-p70b C G C C C T T G G T G C C G G T G T G A A G A A G C G G C G G C A T G G A G A C G A G G A C A C G T  1063

sr-p70a A C T A C C T T C A G G T G C G A G G C C G G G A G A A C T T T G A G A T C C T G A T G A A G C T G  1350
sr-p70f A C T A C C T T C A G G T G C G A G G C C G G G A G A A C T T T G A G A T C C T G A T G A A G C T G  1072
sr-p70d A C T A C C T T C A G G T G C G A G G C C G G G A G A A C T T T G A G A T C C T G A T G A A G C T G   966
sr-p70e A C T A C C T T C A G G T G C G A G G C C G G G A G A A C T T T G A G A T C C T G A T G A A G C T G   966
sr-p70b A C T A C C T T C A G G T G C G A G G C C G G G A G A A C T T T G A G A T C C T G A T G A A G C T G  1113

sr-p70a A A A G A G A G C C T G G A G C T G A T G G A G T T G G T G C C G C A G C C A C T G G T G G A C T C  1400
sr-p70f A A A G A G A G C C T G G A G C T G A T G G A G T T G G T G C C G C A G C C A C T G G T G G A C T C  1122
sr-p70d A A A G A G A G C C T G G A G C T G A T G G A G T T G G T G C C G C A G C C A C T G G T G G A C T C  1016
sr-p70e A A A G A G A G C C T G G A G C T G A T G G A G T T G G T G C C G C A G C C A C T G G T G G A C T C  1016
sr-p70b A A A G A G A G C C T G G A G C T G A T G G A G T T G G T G C C G C A G C C A C T G G T G G A C T C  1163

sr-p70a C T A T C G G C A G C A G C A G C A G C T C C T A C A G A G G C C G A G T C A C C T A C A G C C C C  1450
sr-p70f C T A T C G G C A G C A G C A G C A G C T C C T A C A G A G G C C G A G T C A C C T A C A G C C C C  1172
sr-p70d C T A T C G G C A G C A G C A G C A G C T C C T A C A G A G G C C G A G T C A C C T A C A G C C C C  1066
sr-p70e C T A T C G G C A G C A G C A G C A G C T C C T A C A G A G G C C - - - - - - - - - - - - - - - -  1049
sr-p70b C T A T C G G C A G C A G C A G C A G C T C C T A C A G A G G C C G A G T C A C C T A C A G C C C C  1213

sr-p70a C G T C C T A C G G G C C G G T C C T C T C G C C C A T G A A C A A G G T G C A C G G G G G C A T G  1500
sr-p70f C G T C C T A C G G G C C G G T C C T C T C G C C C A T G A A C A A G G T G C A C G G G G G C A T G  1222
sr-p70d C G T C C T A C G G G C C G G T C C T C T C G C C C A T G A A C A A G G T G C A C G G G G G C A T G  1116
sr-p70e - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1049
sr-p70b C G T C C T A C G G G C C G G T C C T C T C G C C C A T G A A C A A G G T G C A C G G G G G C A T G  1263
```

FIG. 15 cont.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sr-p70f AACAAGCTGCCCTCCGTCAACCAGCTGGTGGGCCAGCCTCCCCCGCACAG 1272
sr-p70d AACAAGCTGCCCTCCGTCAACCAGCTGGTGGGCCAGCCTCCCCCGCACAG 1166
sr-p70e ---------- 1049
sr-p70b AACAAGCTGCCCTCCGTCAACCAGCTGGTGGGCCAGCCTCCCCCGCACAG 1313
sr-p70a TTCGGCAGCTACACCCAACCTGGGGCCCGTGGGCCCCGGGATGCTCAACA 1600
sr-p70f TTCGGCAGCTACACCCAACCTGGGGCCCGTGGGCCCCGGGATGCTCAACA 1322
sr-p70d TTCGGCAGCTACACCCAACCTGGGGCCCGTGGGCCCCGGGATGCTCAACA 1216
sr-p70e ---------- GCCCCGGGATGCTCAACA 1067
sr-p70b TTCGGCAGCTACACCCAACCTGGGGCCCGTGGGCCCCGGGATGCTCAACA 1363
sr-p70a ACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCCACAGC 1650
sr-p70f ACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCCACAGC 1372
sr-p70d ACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCCACAGC 1266
sr-p70e ACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCCACAGC 1117
sr-p70b ACCATGGCCACGCAGTGCCAGCCAACGGCGAGATGAGCAGCAGCCACAGC 1413
sr-p70a GCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCA 1700
sr-p70f GCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCA 1422
sr-p70d GCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCA 1316
sr-p70e GCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCA 1167
sr-p70b GCCCAGTCCATGGTCTCGGGGTCCCACTGCACTCCGCCACCCCCCTACCA 1463
sr-p70a CGCCGACCCCAGCCTCGTCAGTTTTTTAACAGGATTGGGGTGTCCAAACT 1750
sr-p70f CGCCGACCCCAGCCTCGTCAGTTTTTTAACAGGATTGGGGTGTCCAAACT 1472
sr-p70d CGCCGACCCCAGCCTCGTCAGTTTTTTAACAGGATTGGGGTGTCCAAACT 1366
sr-p70e CGCCGACCCCAGCCTCGTC---------- 1186
sr-p70b CGCCGACCCCAGCCTCGTC---------- 1482

FIG. 15 cont.

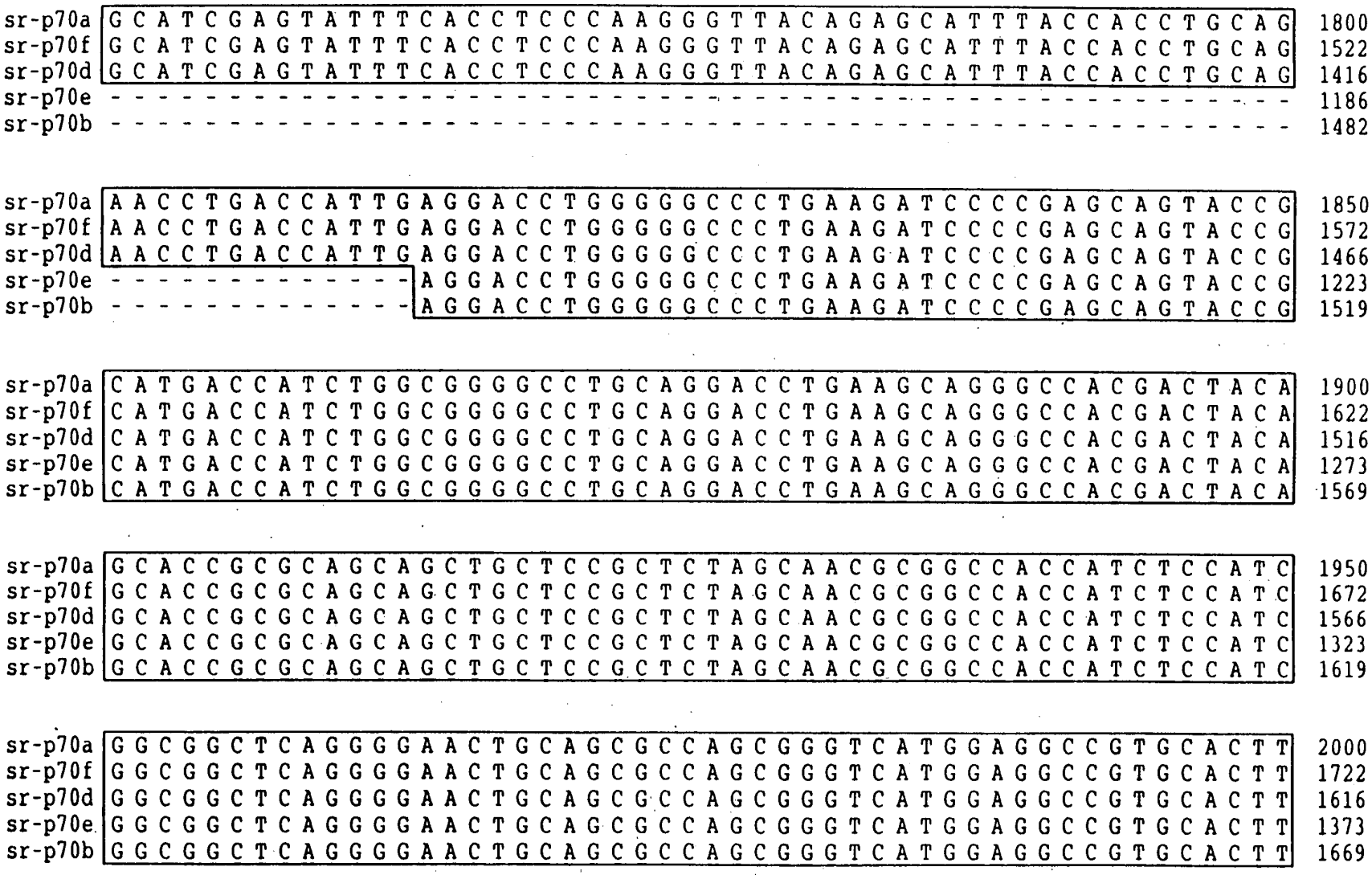

sr-p70a GCATCGAGTATTTCACCTCCCAAGGGTTACAGAGCATTTACCACCTGCAG 1800
sr-p70f GCATCGAGTATTTCACCTCCCAAGGGTTACAGAGCATTTACCACCTGCAG 1522
sr-p70d GCATCGAGTATTTCACCTCCCAAGGGTTACAGAGCATTTACCACCTGCAG 1416
sr-p70e ---------- 1186
sr-p70b ---------- 1482
sr-p70a AACCTGACCATTGAGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTACCG 1850
sr-p70f AACCTGACCATTGAGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTACCG 1572
sr-p70d AACCTGACCATTGAGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTACCG 1466
sr-p70e ----------AGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTACCG 1223
sr-p70b ----------AGGACCTGGGGGCCCTGAAGATCCCCGAGCAGTACCG 1519
sr-p70a CATGACCATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACA 1900
sr-p70f CATGACCATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACA 1622
sr-p70d CATGACCATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACA 1516
sr-p70e CATGACCATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACA 1273
sr-p70b CATGACCATCTGGCGGGGCCTGCAGGACCTGAAGCAGGGCCACGACTACA 1569
sr-p70a GCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCTCCATC 1950
sr-p70f GCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCTCCATC 1672
sr-p70d GCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCTCCATC 1566
sr-p70e GCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCTCCATC 1323
sr-p70b GCACCGCGCAGCAGCTGCTCCGCTCTAGCAACGCGGCCACCATCTCCATC 1619
sr-p70a GGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTT 2000
sr-p70f GGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTT 1722
sr-p70d GGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTT 1616
sr-p70e GGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTT 1373
sr-p70b GGCGGCTCAGGGGAACTGCAGCGCCAGCGGGTCATGGAGGCCGTGCACTT 1669

FIG. 15cont.

```
sr-p70a C C G C G T G C G C C A C A C C A T C A C C A T C C C C A A C C G C G G C G G C C C A G G C G G C G  2050
sr-p70f C C G C G T G C G C C A C A C C A T C A C C A T C C C C A A C C G C G G C G G C C C A G G C G G C G  1772
sr-p70d C C G C G T G C G C C A C A C C A T C A C C A T C C C C A A C C G C G G C G G C C C A G G C G G C G  1666
sr-p70e C C G C G T G C G C C A C A C C A T C A C C A T C C C C A A C C G C G G C G G C C C A G G C G G C G  1423
sr-p70b C C G C G T G C G C C A C A C C A T C A C C A T C C C C A A C C G C G G C G G C C C A G G C G G C G  1719

sr-p70a G C C C T G A C G A G T G G G C G G A C T T C G G C T T C G A C C T G C C C G A C T G C A A G G C C  2100
sr-p70f G C C C T G A C G A G T G G G C G G A C T T C G G C T T C G A C C T G C C C G A C T G C A A G G C C  1822
sr-p70d G C C C T G A C G A G T G G G C G G A C T T C G G C T T C G A C C T G C C C G A C T G C A A G G C C  1716
sr-p70e G C C C T G A C G A G T G G G C G G A C T T C G G C T T C G A C C T G C C C G A C T G C A A G G C C  1473
sr-p70b G C C C T G A C G A G T G G G C G G A C T T C G G C T T C G A C C T G C C C G A C T G C A A G G C C  1769

sr-p70a C G C A A G C A G C C C A T C A A G G A G G A G T T C A C G G A G G C C G A G A T C C A C T G A G G  2150
sr-p70f C G C A A G C A G C C C A T C A A G G A G G A G T T C A C G G A G G C C G A G A T C C A C T G A - -  1870
sr-p70d C G C A A G C A G C C C A T C A A G G A G G A G T T C A C G G A G G C C G A G A T C C A C T G A - -  1764
sr-p70e C G C A A G C A G C C C A T C A A G G A G G A G T T C A C G G A G G C C G A G A T C C A C T G A - -  1521
sr-p70b C G C A A G C A G C C C A T C A A G G A G G A G T T C A C G G A G G C C G A G A T C C A C T G A - -  1817

sr-p70a G C C T C G C C T G G C T G C A G C C T G C G C C A C C G C C C A G A G A C C C A A G C T G C C T C  2200
sr-p70f - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1870
sr-p70d - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1764
sr-p70e - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1521
sr-p70b - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1817

sr-p70a C C C T C T C C T T C C T G T G T G T C C A A A A C T G C C T C A G G A G G C A G G A C C T T C G G  2250
sr-p70f - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1870
sr-p70d - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1764
sr-p70e - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1521
sr-p70b - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1817
```

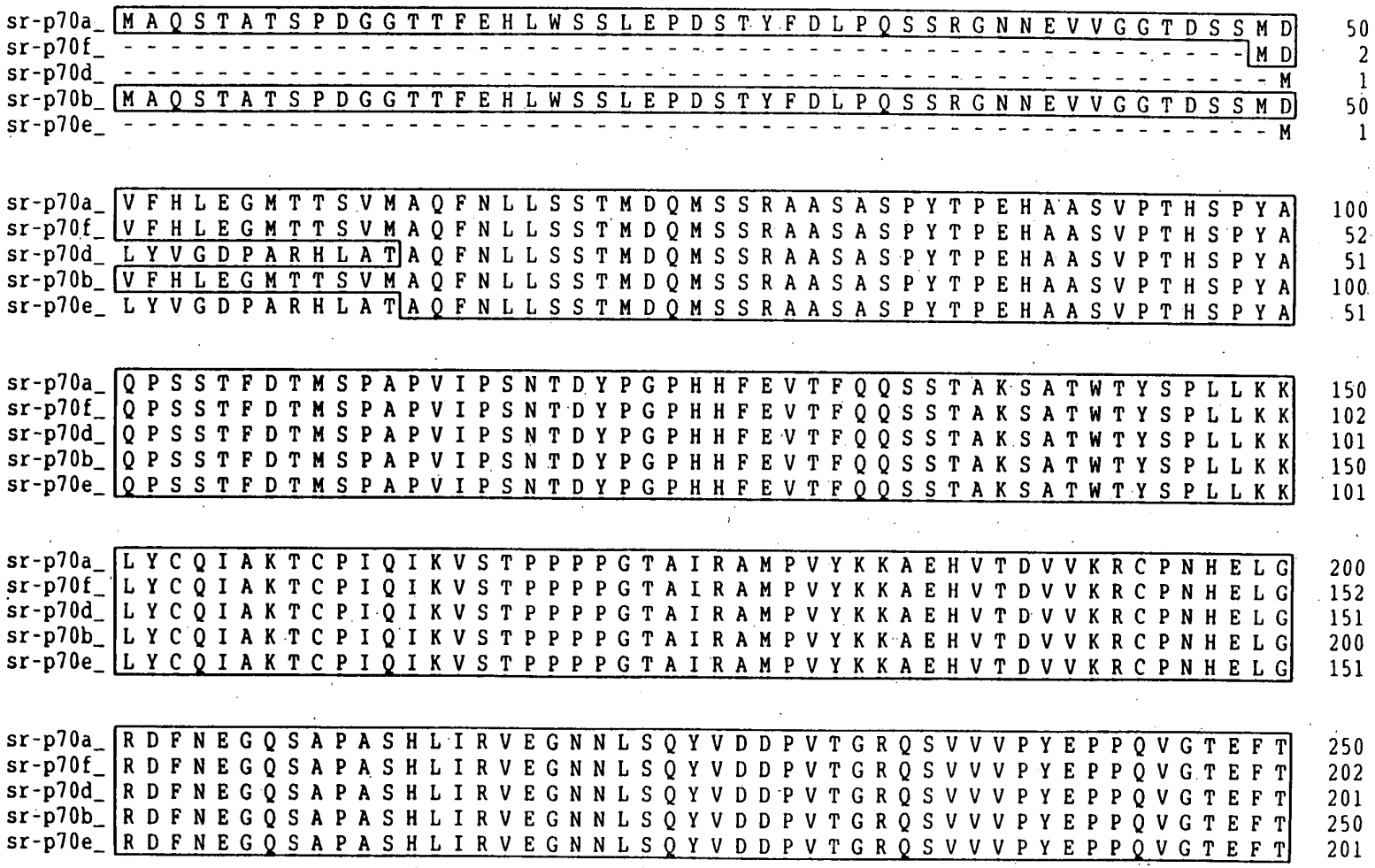
FIG.15 cont.

```
sr-p70a G C T G T G C C C G G G G A A A G G C A A G G T C C G G C C C A T C C C C A G G C A C C T C A C A G  2300
sr-p70f - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1870
sr-p70d - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1764
sr-p70e - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1521
sr-p70b - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1817

sr-p70a G C C C C A G G A A A G G C C C A G C C A C C G A A G C C G C C T G T G G A C A G C C T G A G T C A  2350
sr-p70f - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1870
sr-p70d - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1764
sr-p70e - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1521
sr-p70b - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -  1817

sr-p70a C C T G C A G A A C C                                                                            2361
sr-p70f - - - - - - - - - - -                                                                            1870
sr-p70d - - - - - - - - - - -                                                                            1764
sr-p70e - - - - - - - - - - -                                                                            1521
sr-p70b - - - - - - - - - - -                                                                            1817
```


FIG.15 cont.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sr-p70e_ ----------M 1
sr-p70a_ VFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 100
sr-p70f_ VFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 52
sr-p70d_ LYVGDPARHLATAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 51
sr-p70b_ VFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 100
sr-p70e_ LYVGDPARHLATAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYA 51
sr-p70a_ QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 150
sr-p70f_ QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 102
sr-p70d_ QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 101
sr-p70b_ QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 150
sr-p70e_ QPSSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKK 101
sr-p70a_ LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 200
sr-p70f_ LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 152
sr-p70d_ LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 151
sr-p70b_ LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 200
sr-p70e_ LYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELG 151
sr-p70a_ RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 250
sr-p70f_ RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 202
sr-p70d_ RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 201
sr-p70b_ RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 250
sr-p70e_ RDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFT 201

FIG. 16

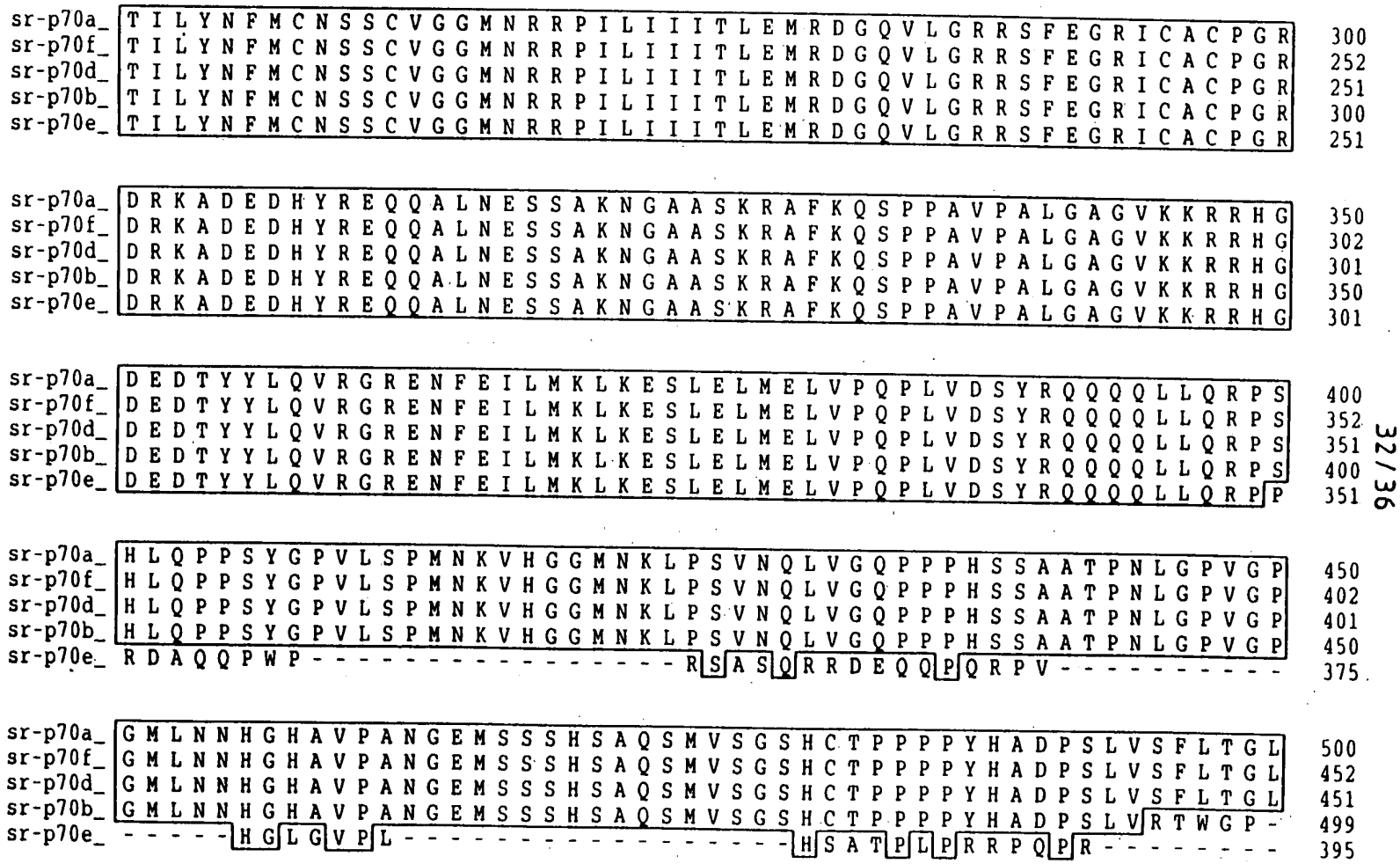


FIG. 16 cont.

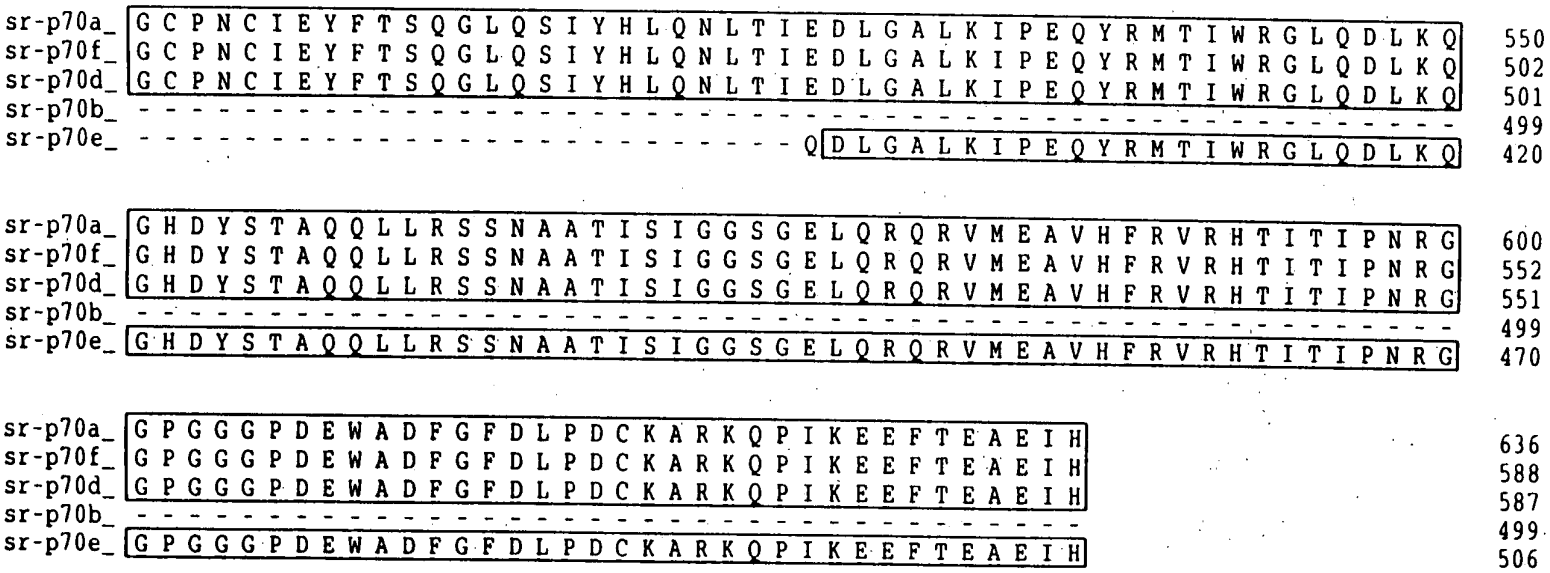
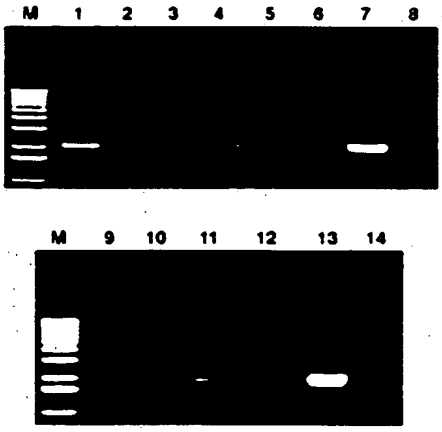

sr-p70a_ G C P N C I E Y F T S Q G L Q S I Y H L Q N L T I E D L G A L K I P E Q Y R M T I W R G L Q D L K Q 550
sr-p70f_ G C P N C I E Y F T S Q G L Q S I Y H L Q N L T I E D L G A L K I P E Q Y R M T I W R G L Q D L K Q 502
sr-p70d_ G C P N C I E Y F T S Q G L Q S I Y H L Q N L T I E D L G A L K I P E Q Y R M T I W R G L Q D L K Q 501
sr-p70b_ 499
sr-p70e_ Q D L G A L K I P E Q Y R M T I W R G L Q D L K Q 420
sr-p70a_ G H D Y S T A Q Q L L R S S N A A T I S I G G S G E L Q R Q R V M E A V H F R V R H T I T I P N R G 600
sr-p70f_ G H D Y S T A Q Q L L R S S N A A T I S I G G S G E L Q R Q R V M E A V H F R V R H T I T I P N R G 552
sr-p70d_ G H D Y S T A Q Q L L R S S N A A T I S I G G S G E L Q R Q R V M E A V H F R V R H T I T I P N R G 551
sr-p70b_ 499
sr-p70e_ G H D Y S T A Q Q L L R S S N A A T I S I G G S G E L Q R Q R V M E A V H F R V R H T I T I P N R G 470
sr-p70a_ G P G G G P D E W A D F G F D L P D C K A R K Q P I K E E F T E A E I H 636
sr-p70f_ G P G G G P D E W A D F G F D L P D C K A R K Q P I K E E F T E A E I H 588
sr-p70d_ G P G G G P D E W A D F G F D L P D C K A R K Q P I K E E F T E A E I H 587
sr-p70b_ 499
sr-p70e_ G P G G G P D E W A D F G F D L P D C K A R K Q P I K E E F T E A E I H 506

FIG.16 cont.

```
  1  TAACGCCCGCGGCCGCCTACTCCCCGCGGCGCCTCCCCTCCCCGCGCCCATATAACCCGC   60
 61  CTAGGGGCCGGGCAGCCCGCCCTGCCTCCCCGCCCGCGCACCCGCCCGGAGGCTCGCGCG  120
121  CCCGCGAAGGGGACGCAGCGAAACCGGGGCCCGCGCCAGGCCAGCCGGGACGGACGCCGA  180
181  TGCCCGGGGCTGCGACGGCTGCAGAGCAAGCTGCCCTTGGAGGCCGGCGTGGGGAAGATG  240
                                                          M     1
241  GCCCAGTCCACCGCCACCTCCCCTGATGGGGGCACCACGTTTGAGCACCTCTGGAGCTCT  300
  2  A  Q  S  T  A  T  S  P  D  G  G  T  T  F  E  H  L  W  S  S    21
301  CTGGAACCAGACAGCACCTACTTCGACCTTCCCCAGTCAAGCCGGGGGAATAATGAGGTG  360
 22  L  E  P  D  S  T  Y  F  D  L  P  Q  S  S  R  G  N  N  E  V    41
361  GTGGGCGGAACGGATTCCAGCATGGACGTCTTCCACCTGGAGGGCATGActACATCTGTC  420
 42  V  G  G  T  D  S  S  M  D  V  F  H  L  E  G  M  T  T  S  V    61
421  ATGGCCCAGTTCAATCTGCTGAGCAGCACCATGGACCAGATGAGCAGCCGCGCGGCCTCG  480
 62  M  A  Q  F  N  L  L  S  S  T  M  D  Q  M  S  S  R  A  A  S    81
481  GCCAGCCCCTACACCCCAGAGCACGCCGCCAGCGTGCCCACCCACTCGCCCTACGCACAA  540
 82  A  S  P  Y  T  P  E  H  A  A  S  V  P  T  H  S  P  Y  A  Q   101
541  CCCAGCTCCACCTTCGACACCATGTCGCCGGCGCCTGTCATCCCCTCCAACACCGACTAC  600
102  P  S  S  T  F  D  T  M  S  P  A  P  V  I  P  S  N  T  D  Y   121
601  CCCGGACCCCACCACTTTGAGGTCACTTTCCAGCAGTCCAGCACGGCCAAGTCAGCCACC  660
122  P  G  P  H  H  F  E  V  T  F  Q  Q  S  S  T  A  K  S  A  T   141
661  TGGACGTA......
142  W  T     .  .
```

FIG. 17

FIG. 18



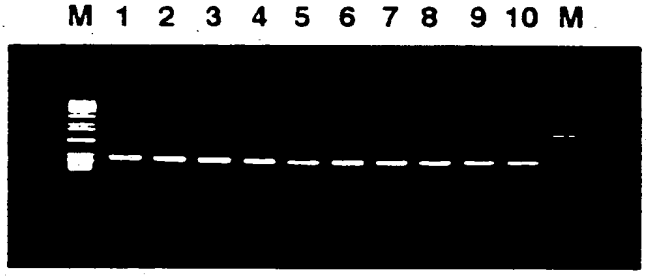


FIG. 19A

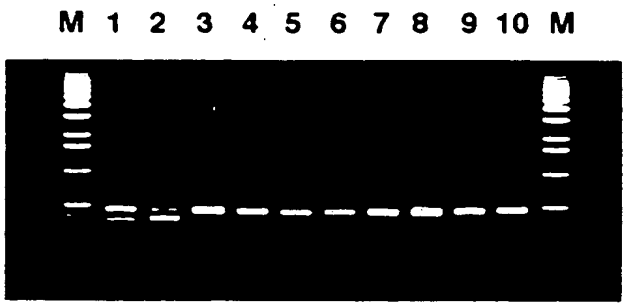


FIG. 19B

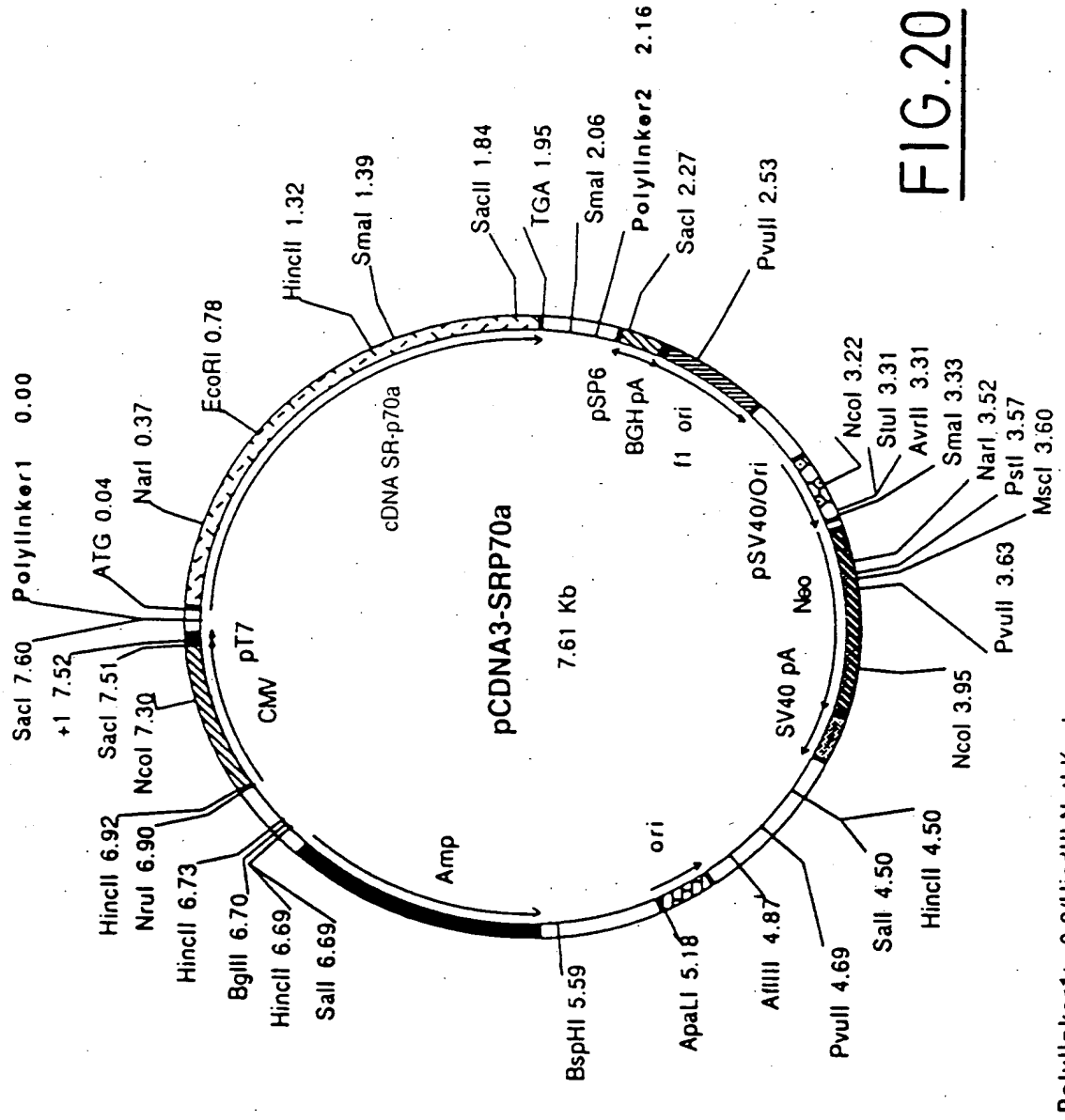


FIG.20

PolyIlnker1: 0.0/HindIII.NotI.KpnI.
PolyIlnker2: 2.16/XbaI.NotI.ApaI.